

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 8, 2006, 19:37:09 ; Search time 246 Seconds  
(without alignments)  
897.684 Million cell updates/sec

Title: US-10-063-595-88  
Perfect score: 1747  
Sequence: 1 MNQLSFLFLFIATTRGWSTD.....HVGYSRSSREITEAAVLLFYR 313

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Uniprot\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1747	100.0	313	2	QSIWS5_HUMAN	Q5iws5 homo sapien
2	1738	99.5	313	1	ITLNL_HUMAN	Q8wwa0 homo sapien
3	1738	99.5	313	2	Q5VYI4_HUMAN	Q5vyi4 homo sapien
4	1733	99.2	313	2	QSIWS4_HUMAN	Q5iws4 homo sapien
5	1449.5	83.0	325	1	ITLN2_HUMAN	Q8wwu7 homo sapien
6	1449.5	83.0	325	2	QSVYI0_HUMAN	Q5vyi0 homo sapien
7	1427	81.7	313	1	ITLIA_MOUSE	Q88310 mus musculus
8	1427	81.7	313	2	QSIWS3_MOUSE	Q5iws3 mus musculus
9	1391	79.6	313	1	ITLIB_MOUSE	Q80za0 mus musculus
10	1129	64.6	339	2	Q6P7Y6_XENTR	Q6p7y6 xenopus lae
11	1105.5	63.3	338	2	Q8JJD0_XENLA	Q8jjd0 xenopus lae
12	1103	63.1	342	2	Q800K0_XENLA	Q800k0 xenopus lae
13	1095	62.7	339	2	Q5PPM0_XENLA	Q5ppm0 xenopus lae
14	1080	61.8	315	2	Q8JJC9_XENLA	Q8jjc9 xenopus lae
15	1049.5	60.1	313	2	Q91719_XENLA	Q91719 xenopus lae
16	1049	60.0	285	2	Q6GR52_XENLA	Q6gr52 xenopus lae
17	1047.5	60.0	320	2	Q5U4L0_XENLA	Q5u4l0 xenopus lae
18	1044.5	59.8	313	2	P79957_XENLA	P79957 xenopus lae
19	1034	59.2	321	2	Q6GP37_XENLA	Q6gp37 xenopus lae
20	1025	58.7	320	2	Q8AWX0_XENTR	Q8awx0 xenopus tro
21	892	51.1	333	2	Q98TC9_LAMJA	Q98tc9 lampetra ja
22	873	50.0	318	2	Q4U122_CTEID	Q4ul22 ctenopharyn
23	870	49.8	318	2	Q4U121_CTEID	Q4ul21 ctenopharyn
24	820.5	47.0	320	2	Q4W8M6_LAMJA	Q4w8m6 lampetra ja
25	755	43.2	256	2	Q6DEN7_XENTR	Q6den7 xenopus tro
26	347.5	19.9	579	2	Q69HM9_CIOIN	Q69hm9 ciona intes
27	293.5	16.8	121	2	Q9DFE0_ONCMY	Q9dfe0 oncorhynchu
28	129.5	7.4	282	1	FIBA_PARPA	P19477 parastichop
29	125.5	7.2	475	2	Q6MK33_BDEBA	Q6mk33 bdellovibri
30	125	7.2	488	2	Q6MK34_BDEBA	Q6mk34 bdellovibri
31	119.5	6.8	485	2	Q6NYE1_BRARE	Q6nye1 brachydanio

32	115.5	6.6	457	2	Q5XK91_XENLA	Q5xk91 xenopus lae
33	111.5	6.4	1946	2	Q4S290_TETNG	Q4s290 tetraodon n
34	110.5	6.3	451	2	Q5TYU3_BRARE	Q5tyu3 brachydanio
35	110.5	6.3	525	2	Q4LES0_BRARE	Q4les0 brachydanio
36	110.5	6.3	1296	2	Q70HX0_MOUSE	Q70hx0 mus musculus
37	109.5	6.3	189	2	Q5HX51_CAMJR	Q5hx51 campylobact
38	109.5	6.3	1560	1	TENN_MOUSE	Q80z71 mus musculus
39	109	6.2	306	2	Q5EAM5_XENTR	Q5eam5 xenopus tro
40	109	6.2	491	1	FIBB_HUMAN	P02675 homo sapien
41	109	6.2	491	2	Q5R535_PONPY	Q5r535 pongo pygma
42	107.5	6.2	1243	2	Q9UVC1_CLAFU	Q9uvc1 cladosporiu
43	107	6.1	310	2	Q7QHK2_ANOGA	Q7qhk2 anopheles g
44	106.5	6.1	246	2	Q9V7U5_DROME	Q9v7u5 drosophila
45	106.5	6.1	318	2	Q5BKK1_XENTR	Q5bkk1 xenopus tro
46	106.5	6.1	649	2	Q7VY64_BORPE	Q7vy64 bordetella
47	106.5	6.1	649	2	Q7W912_BORPA	Q7w912 bordetella
48	106.5	6.1	649	2	Q7WKF7_BORBR	Q7wkf7 bordetella
49	106	6.1	1294	1	TENN_HUMAN	Q9uqp3 homo sapien
50	106	6.1	1299	2	Q5R360_HUMAN	Q5r360 homo sapien
51	105.5	6.0	189	2	Q9RJ12_CAMJE	Q9pj12 campylobact
52	105.5	6.0	269	2	Q8BL54_MOUSE	Q8bl54 mus musculus
53	105.5	6.0	616	2	O16770_CABEL	O16770 caenorhabdi
54	105	6.0	434	2	O52730_9BACI	O52730 bacillus sp
55	104.5	6.0	270	2	Q91332_RANSY	Q91332 rana sylvat
56	104.5	6.0	426	2	Q5XMX6_9HEPC	Q5xmx6 hepatitis c
57	104.5	6.0	427	2	Q4SEZ4_TETNG	Q4sez4 tetraodon n
58	103.5	5.9	190	2	Q4HFP0_CAMCO	Q4hfp0 campylobact
59	103.5	5.9	426	2	Q5XMY0_9HEPC	Q5xmy0 hepatitis c
60	103.5	5.9	426	2	Q5XMY3_9HEPC	Q5xmy3 hepatitis c
61	103.5	5.9	426	2	Q5XMY5_9HEPC	Q5xmy5 hepatitis c
62	103.5	5.9	1917	2	Q51ED6_ENTHI	Q51ed6 entamoeba h
63	103.5	5.9	2301	2	Q95Z81_9UROC	Q95z81 oikopleura
64	103	5.9	337	2	Q9BE00_MACFA	Q9be00 macaca fasc
65	103	5.9	429	2	Q8TTF0_METAC	Q8ttf0 methanosarc
66	103	5.9	470	2	Q4S2B3_TETNG	Q4s2b3 tetraodon n
67	102.5	5.9	426	2	Q5XMY4_9HEPC	Q5xmy4 hepatitis c
68	102.5	5.9	457	2	Q6AX44_XENLA	Q6ax44 xenopus lae
69	102.5	5.9	592	2	Q7UJX1_RHOBA	Q7ujx1 rhodopirell
70	102	5.8	481	1	FIBB_MOUSE	Q8k0e8 mus musculus
71	102	5.8	481	2	Q5R6W8_PONPY	Q5r6w8 pongo pygma
72	102	5.8	550	2	Q74FD5_GEOSL	Q74fd5 geobacter s
73	101.5	5.8	269	2	Q8BJE7_MOUSE	Q8bje7 mus musculus
74	101.5	5.8	280	2	O93526_CHICK	O93526 gallus gall
75	101.5	5.8	399	2	Q4WKU8_ASPFU	Q4wku8 aspergillus
76	101.5	5.8	426	2	Q5XMX8_9HEPC	Q5xmx8 hepatitis c
77	101.5	5.8	426	2	Q5XMY1_9HEPC	Q5xmy1 hepatitis c
78	101.5	5.8	426	2	Q5XMZ4_9HEPC	Q5xmx4 hepatitis c
79	101.5	5.8	459	2	Q6P9R8_MOUSE	Q6p9r8 mus musculus
80	101.5	5.8	680	2	Q8EDZ3_SHEON	Q8edz3 shewanella
81	101	5.8	363	2	Q9VF34_DROME	Q9vtf34 drosophila
82	101	5.8	427	2	Q86H02_BIOGL	Q86h02 biomphalari
83	101	5.8	732	2	Q86H03_BIOGL	Q86h03 biomphalari
84	100.5	5.8	426	2	Q5XMY2_9HEPC	Q5xmy2 hepatitis c
85	100.5	5.8	426	2	Q5XMY8_9HEPC	Q5xmy8 hepatitis c
86	100.5	5.8	426	2	Q5XMZ5_9HEPC	Q5xmx5 hepatitis c
87	100.5	5.8	426	2	Q5XMZ6_9HEPC	Q5xmx6 hepatitis c
88	100.5	5.8	655	2	Q86H06_BIOGL	Q86h06 biomphalari
89	100	5.7	572	2	Q8B9F4_NPVRO	Q8b9f4 rachiplusia
90	100	5.7	796	2	Q6V2E1_ENTAS	Q6v2e1 enterobacte
91	100	5.7	2265	1	FINC_BOVIN	P07589 bos taurus
92	99.5	5.7	318	2	Q5U490_XENLA	Q5u490 xenopus lae
93	99.5	5.7	318	2	Q7ZT74_XENLA	Q7zt74 xenopus lae
94	99.5	5.7	426	2	Q5XMX7_9HEPC	Q5xmx7 hepatitis c
95	99.5	5.7	2752	2	Q61TE9_CAEBR	Q61te9 caenorhabdi
96	99	5.7	274	2	Q57S28_SALCH	Q57s28 salmonella
97	99	5.7	274	2	Q8ZR67_SALTY	Q8zr67 salmonella
98	99	5.7	279	2	Q7YXN0_ORNMO	Q7yxm0 ornithodoro
99	99	5.7	308	2	Q5XG23_XENLA	Q5xg23 xenopus lae
100	99	5.7	308	2	Q7ZT75_XENLA	Q7zt75 xenopus lae
101	99	5.7	375	1	ANGP2_BOVIN	Q77802 bos taurus
102	99	5.7	444	1	FIBG_BOVIN	P12799 bos taurus
103	99	5.7	460	1	ANGL3_HUMAN	Q9y5c1 homo sapien
104	99	5.7	460	2	Q5TAX7_HUMAN	Q5tax7 homo sapien

105	99	5.7	466	2	Q4T9V4_TETNG	Q4t9v4 tetraodon n	178	93.5	5.4	1701	2	Q9V3E8_DROME	Q9v3e8 drosophila
106	99	5.7	479	1	FIBB_RAT	P14480 rattus norv	179	93	5.3	314	2	Q8VC25_MOUSE	Q8vc25 mus musculu
107	99	5.7	479	2	Q5I0P7_RAT	Q5i0p7 rattus norv	180	93	5.3	314	2	Q71KU9_MOUSE	Q71ku9 mus musculu
108	99	5.7	503	2	Q7TME5_RAT	Q7tme5 rattus norv	181	93	5.3	364	2	Q5B8S7_EMENI	Q5b8s7 aspergillus
109	99	5.7	796	1	DHG_ECOLI	P15877 escherichia	182	93	5.3	468	1	FIBB_BOVIN	P02676 bos taurus
110	99	5.7	796	2	Q8X946_ECO57	Q8x946 escherichia	183	93	5.3	536	2	Q7V8Q0_PROMM	Q7v8q0 prochloroco
111	99	5.7	802	2	Q8FL38_ECOL6	Q8fl38 escherichia	184	92.5	5.3	218	2	Q6UY50_HUMAN	Q6uy50 homo sapien
112	98.5	5.6	259	2	Q7QHK6_ANOGA	Q7qhk6 anopheles g	185	92.5	5.3	279	2	Q6JJK9_9DIPT	Q6jkk9 armigeres s
113	98.5	5.6	426	2	Q5XMK5_9HEPC	Q5xmk5 hepatitis c	186	92.5	5.3	288	2	Q6UXM4_HUMAN	Q6uxm4 homo sapien
114	98.5	5.6	426	2	Q5XMY6_9HEPC	Q5xmy6 hepatitis c	187	92.5	5.3	299	1	FCN3_HUMAN	Q75636 homo sapien
115	98.5	5.6	426	2	Q5XMZ1_9HEPC	Q5xmz1 hepatitis c	188	92.5	5.3	299	2	Q6IBJ5_HUMAN	Q6ibj5 homo sapien
116	98.5	5.6	426	2	Q5XMZ2_9HEPC	Q5xmz2 hepatitis c	189	92.5	5.3	348	2	Q4SFS2_TETNG	Q4sfs2 tetraodon n
117	98.5	5.6	462	2	Q6E7H1_PIG	Q6e7h1 sus scrofa	190	92.5	5.3	426	2	Q5XMR8_9HEPC	Q5xmr8 hepatitis c
118	98.5	5.6	510	2	Q4SIU0_TETNG	Q4siu0 tetraodon n	191	92.5	5.3	426	2	Q5XMT7_9HEPC	Q5xmt7 hepatitis c
119	98.5	5.6	652	2	Q9NDQ1_CIOIN	Q9ndq1 ciona intes	192	92.5	5.3	426	2	Q5XMZ0_9HEPC	Q5xmz0 hepatitis c
120	98.5	5.6	725	2	Q9JXU3_NEIMB	Q9jxu3 neisseria m	193	92.5	5.3	426	2	Q5XMZ3_9HEPC	Q5xmz3 hepatitis c
121	98.5	5.6	777	2	Q7QHLO_ANOGA	Q7qhl0 anopheles g	194	92.5	5.3	490	1	ANGL1_MOUSE	Q640p2 mus musculu
122	98	5.6	481	2	Q5R975_PONPY	Q5r975 pongo pygma	195	92.5	5.3	576	2	Q4KP46_9HEPC	Q4kp46 hepatitis c
123	98	5.6	776	2	Q83SM2_SHIFL	Q83sm2 shigella fl	196	92.5	5.3	694	2	Q87TP9_VIBPA	Q87tp9 vibrio para
124	98	5.6	796	2	Q7UDR6_SHIFL	Q7udr6 shigella fl	197	92.5	5.3	1077	2	Q977X0_METMA	Q977x0 methanosarc
125	97.5	5.6	324	2	Q95P99_HALRO	Q95p99 halocynthia	198	92.5	5.3	1077	2	Q977X1_METMA	Q977x1 methanosarc
126	97.5	5.6	426	2	Q5XMR7_9HEPC	Q5xmr7 hepatitis c	199	92.5	5.3	1095	2	Q8PKS2_METMA	Q8pxs2 methanosarc
127	97.5	5.6	426	2	Q5XMS4_9HEPC	Q5xms4 hepatitis c	200	92.5	5.3	1319	2	O45599_CAEEL	O45599 caenorhabdi
128	97.5	5.6	426	2	Q5XMK9_9HEPC	Q5xmk9 hepatitis c	201	92.5	5.3	1324	2	Q4RJ05_TETNG	Q4rj05 tetraodon n
129	97.5	5.6	426	2	Q5XMS2_9HEPC	Q5xms2 hepatitis c	202	92.5	5.3	1710	2	Q4FAI8_BRARE	Q4fai8 brachydanio
130	97.5	5.6	431	2	Q95LU3_MACFA	Q95lu3 macaca fasc	203	92	5.3	314	2	Q5M8C6_RAT	Q5m8c6 rattus norv
131	97.5	5.6	496	1	ANGP2_PIG	Q9bdy7 sus scrofa	204	92	5.3	321	2	Q5M8W6_XENTR	Q5m8w6 xenopus tro
132	97.5	5.6	509	1	ANGP4_MOUSE	Q9wvh6 mus musculu	205	92	5.3	421	2	Q95UV8_BIOGL	Q95uv8 biophalari
133	97.5	5.6	627	2	Q60UV5_CAEBR	Q60uv5 caenorhabdi	206	92	5.3	484	2	Q4RHE8_TETNG	Q4rhe8 tetraodon n
134	97	5.6	495	1	CROM_OCTDO	P30841 octopus dof	207	92	5.3	496	1	ANGP2_HUMAN	O15123 homo sapien
135	96.5	5.5	318	2	Q7ZT72_XENLA	Q7zt72 xenopus lae	208	92	5.3	796	2	Q8Z9E0_SALT1	Q8z9e0 salmonella
136	96.5	5.5	426	2	Q5XMR6_9HEPC	Q5xmr6 hepatitis c	209	91.5	5.2	194	2	Q4HM23_CAMLA	Q4hm23 campylobact
137	96.5	5.5	426	2	Q5XMR9_9HEPC	Q5xmr9 hepatitis c	210	91.5	5.2	280	2	Q6VFG6_ANOGA	Q6vfg6 anopheles g
138	96.5	5.5	426	2	Q5XMS0_9HEPC	Q5xms0 hepatitis c	211	91.5	5.2	321	2	Q4WYX7_ASFPU	Q4wyx7 aspergillus
139	96.5	5.5	426	2	Q5XMS2_9HEPC	Q5xms2 hepatitis c	212	91.5	5.2	426	2	Q5XND9_9HEPC	Q5xnd9 hepatitis c
140	96.5	5.5	461	2	Q6UXK6_HUMAN	Q6uxk6 homo sapien	213	91.5	5.2	619	1	CHIT_STRLI	P36909 streptomyce
141	96.5	5.5	461	2	Q8N539_HUMAN	Q8n539 homo sapien	214	91.5	5.2	1646	2	Q4PQU3_9HEPC	Q4pqu3 hepatitis c
142	96.5	5.5	496	1	ANGP2_MOUSE	O35608 mus musculu	215	91.5	5.2	1840	2	Q59IP3_PIG	Q59ip3 sus scrofa
143	96.5	5.5	3700	2	Q4KAE3_PSEF5	Q4kae3 pseudomonas	216	91	5.2	324	2	Q95PA0_HALRO	Q95pa0 halocynthia
144	96	5.5	1746	2	Q5GZI6_XANOR	Q5gzi6 xanthomonas	217	91	5.2	325	2	Q8D555_VIBVU	Q8d555 vibrio vuln
145	96	5.5	3010	2	Q91AU0_9HEPC	Q91au0 hepatitis c	218	91	5.2	464	2	Q9AZ86_9CAUD	Q9az86 lactobacill
146	95.5	5.5	280	2	Q6VFG8_ANOGA	Q6vfg8 anopheles g	219	91	5.2	493	1	ANGL2_MOUSE	Q9r045 mus musculu
147	95.5	5.5	338	2	Q4SY92_TETNG	Q4sy92 tetraodon n	220	91	5.2	493	2	Q9JU03_RAT	Q9jj03 rattus norv
148	95.5	5.5	363	2	Q7QHI4_ANOGA	Q7qhi4 anopheles g	221	91	5.2	493	2	Q8BM09_MOUSE	Q8bm09 mus musculu
149	95.5	5.5	426	2	Q5XMS1_9HEPC	Q5xms1 hepatitis c	222	91	5.2	501	2	Q4PE59_USTMA	Q4pe59 ustilago ma
150	95.5	5.5	450	1	UTH1_YEAST	P36135 saccharomyc	223	91	5.2	626	2	Q9H0I9_HUMAN	Q9h0i9 homo sapien
151	95.5	5.5	463	1	FIBB_CHICK	Q02020 gallus gall	224	91	5.2	626	2	Q96M82_HUMAN	Q96m82 homo sapien
152	95.5	5.5	477	1	FIBB_PETMA	P02678 petromyzon	225	91	5.2	642	2	Q61EH5_CAEBR	Q61eh5 caenorhabdi
153	95.5	5.5	502	2	Q4RHP0_TETNG	Q4rhp0 tetraodon n	226	91	5.2	733	2	Q5V334_HALMA	Q5v334 haloarcula
154	95	5.4	576	2	Q4KP41_9HEPC	Q4kp41 hepatitis c	227	91	5.2	836	2	Q5NRA2_ZYMMO	Q5nra2 zymomonas m
155	95	5.4	725	2	Q9JW26_NEIMA	Q9jw26 neisseria m	228	91	5.2	1778	2	Q8EF34_SHEON	Q8ef34 shewanella
156	94.5	5.4	347	2	Q5K9X7_CRYNE	Q5k9x7 cryptococcu	229	91	5.2	3010	2	Q55P04_CRYNE	Q55p04 cryptococcu
157	94.5	5.4	372	2	Q55JM4_CRYNE	Q55jm4 cryptococcu	230	90.5	5.2	220	2	Q9QIX1_9HEPC	Q9qix1 hepatitis c
158	94.5	5.4	413	2	O18544_BIOGL	O18544 biophalari	231	90.5	5.2	244	2	Q8T8A2_CIOSA	Q8t8a2 ciona savig
159	94.5	5.4	614	2	Q90484_BRARE	Q90484 brachydanio	232	90.5	5.2	244	2	Q9HBP3_HUMAN	Q9hbp3 homo sapien
160	94.5	5.4	649	2	Q97U94_SULSO	Q97u94 sulfolobus	233	90.5	5.2	279	2	Q5YD77_9ARAC	Q5yd77 loxosceles
161	94.5	5.4	685	2	Q6D2W3_ERWCT	Q6d2w3 erwinia car	234	90.5	5.2	296	2	Q7QHN9_ANOGA	Q7qhn9 anopheles g
162	94.5	5.4	1203	2	Q86XZ0_DICDI	Q86kz0 dictyosteli	235	90.5	5.2	426	2	Q5XNE3_9HEPC	Q5xne3 hepatitis c
163	94	5.4	325	2	Q87FH2_VIBPA	Q87fh2 vibrio para	236	90.5	5.2	426	2	Q5XNE3_9HEPC	Q5xne3 hepatitis c
164	94	5.4	338	2	Q5XJQ0_BRARE	Q5xjq0 brachydanio	237	90.5	5.2	429	2	Q5U565_XENLA	Q5u565 xenopus lae
165	94	5.4	453	2	Q8CED0_MOUSE	Q8ced0 mus musculu	238	90.5	5.2	576	2	Q4KP50_9HEPC	Q4kp50 hepatitis c
166	94	5.4	484	2	Q5JHH5_PYRKO	Q5jhh5 pyrococcus	239	90.5	5.2	876	2	Q9LAJ2_CLOCL	Q9laj2 clostridium
167	94	5.4	511	2	Q4FKK6_9TRYP	Q4fkk6 trypanosoma	240	90.5	5.2	1644	2	Q4PQU6_9HEPC	Q4pqu6 hepatitis c
168	94	5.4	1018	2	Q8YK71_ANASP	Q8yk71 anabaena sp	241	90.5	5.2	1899	2	Q54YJ1_DICDI	Q54yj1 dictyosteli
169	94	5.4	1778	2	Q5KEF3_CRYNE	Q5kef3 cryptococcu	242	90.5	5.2	2742	2	Q5UL15_9HEPC	Q5ul15 hepatitis c
170	93.5	5.4	413	2	Q7VK58_HELHP	Q7vk58 helicobacte	243	90.5	5.2	2742	2	Q5UL16_9HEPC	Q5ul16 hepatitis c
171	93.5	5.4	426	2	Q5XMT5_9HEPC	Q5xmt5 hepatitis c	244	90	5.2	191	2	Q9EW89_STROI	Q9ew89 streptomyc
172	93.5	5.4	426	2	Q5XMT6_9HEPC	Q5xmt6 hepatitis c	245	90	5.2	198	2	Q8SYS3_DROME	Q8sys3 drosophila
173	93.5	5.4	426	2	Q5XMT9_9HEPC	Q5xmt9 hepatitis c	246	90	5.2	325	2	Q7MBZ2_VIBVY	Q7mbz2 vibrio vuln
174	93.5	5.4	426	2	Q5XN45_9HEPC	Q5xn45 hepatitis c	247	90	5.2	372	2	O18545_BIOGL	O18545 biophalari
175	93.5	5.4	426	2	Q5XN48_9HEPC	Q5xn48 hepatitis c	248	90	5.2	385	2	Q95UV9_BIOGL	Q95uv9 biophalari
176	93.5	5.4	489	2	Q5KQT8_BRARE	Q5kqt8 brachydanio	249	90	5.2	426	2	Q5XNJ8_9HEPC	Q5xnj8 hepatitis c
177	93.5	5.4	551	1	AMYB_THETU	P19584 thermoanaer	250	90	5.2	510	2	Q5KQT9_BRARE	Q5kqt9 brachydanio





397	86	4.9	441	2	Q9DER0_CHICK	Q9der0 gallus gall	470	85	4.9	649	2	Q4IP88_GIBZE	Q4ipe8 gibberella
398	86	4.9	450	2	Q67119_9INFA	Q67119 influenza a	471	85	4.9	670	2	Q419J1_GIBZE	Q419j1 gibberella
399	86	4.9	493	2	Q9DER2_CHICK	Q9der2 gallus gall	472	85	4.9	687	2	Q663W5_YERPS	Q663w5 versinia ps
400	86	4.9	564	1	HEMA_IASE2	P19701 influenza a	473	85	4.9	764	2	Q9WYE4_THEMA	Q9wye4 thermotoga
401	86	4.9	575	2	Q89GX5_BRAJA	Q89gx5 bradyrhizob	474	85	4.9	840	2	Q8FDY6_ECOL6	Q8fdy6 escherichia
402	86	4.9	662	2	Q4YRF7_PLABE	Q4yrf7 plasmodium	475	85	4.9	843	2	Q8FAQ3_ECOL6	Q8faq3 escherichia
403	86	4.9	792	2	Q7NNR7_GLOVI	Q7nnr7 gloeobacter	476	85	4.9	971	2	Q68XX4_RICTY	Q68xx4 rickettsia
404	86	4.9	1028	2	Q8A580_BACTN	Q8a580 bacteroides	477	85	4.9	999	2	Q8A365_BACTN	Q8a365 bacteroides
405	86	4.9	1230	2	Q4N8Y9_THEPA	Q4n8y9 theileria p	478	85	4.9	1011	2	Q4WG05_ASPFU	Q4wg05 aspergillus
406	86	4.9	1356	1	TENR_RAT	Q05546 rattus norv	479	85	4.9	1358	1	TENR_MOUSE	Q8byi9 mus musculu
407	86	4.9	1391	2	Q4SYC9_TETNG	Q05546 rattus norv	480	85	4.9	2472	2	Q14214_HUMAN	Q14214 homo sapien
408	86	4.9	1453	2	Q755D1_ASHGO	Q755d1 ashbya gos	481	85	4.9	2796	1	CSMD3_MOUSE	Q80t79 mus musculu
409	86	4.9	1968	2	Q5QG18_LACRE	Q5gg18 lactobacill	482	85	4.9	2809	1	FBN3_HUMAN	Q75n90 homo sapien
410	86	4.9	2179	1	K0310_HUMAN	Q15027 homo sapien	483	85	4.9	3867	2	Q53Q02_HUMAN	Q53qq2 homo sapien
411	85.5	4.9	228	2	Q8EL80_OCEIH	Q8el80 oceanobacil	484	85	4.9	6669	1	NEBU_HUMAN	Q72u30 leptospira
412	85.5	4.9	358	1	GLNA_CRYNE	Q96u99 cryptococcu	485	84.5	4.8	197	2	Q72U30_LEPIC	Q5spp3 brachydanio
413	85.5	4.9	358	2	Q55ZS0_CRYNE	Q55z80 cryptococcu	486	84.5	4.8	231	2	Q5SPP3_BRARE	Q31l176 neisseria m
414	85.5	4.9	374	1	OMPF_SERMA	Q33980 serratia ma	487	84.5	4.8	237	2	Q31176_NEIME	Q7xh46 oryza sativ
415	85.5	4.9	426	2	Q5XN26_9HEPC	Q5xn26 hepatitis c	488	84.5	4.8	278	2	Q7XH46_ORYSA	Q8s5d6 oryza sativ
416	85.5	4.9	426	2	Q5XN42_9HEPC	Q5xn42 hepatitis c	489	84.5	4.8	278	2	Q8S5D6_ORYSA	Q7xkc3 oryza sativ
417	85.5	4.9	426	2	Q5XN52_9HEPC	Q5xn52 hepatitis c	490	84.5	4.8	318	2	Q8S5D6_ORYSA	Q5ba96 aspergillus
418	85.5	4.9	426	2	Q5XN73_9HEPC	Q5xn73 hepatitis c	491	84.5	4.8	380	2	Q5BA96_EMENI	Q8ey32 leptospira
419	85.5	4.9	426	2	Q5XN76_9HEPC	Q5xn76 hepatitis c	492	84.5	4.8	380	2	Q8EY32_LEPIN	Q9gni8 caenorhabdi
420	85.5	4.9	426	2	Q5XN91_9HEPC	Q5xn91 hepatitis c	493	84.5	4.8	390	2	Q9GNI8_CAEEL	Q90689 gallus gall
421	85.5	4.9	426	2	Q5XNE0_9HEPC	Q5xne0 hepatitis c	494	84.5	4.8	399	2	Q5LGUI_BACFN	Q64xp3 bacteroides
422	85.5	4.9	426	2	Q5XNE4_9HEPC	Q5xne4 hepatitis c	495	84.5	4.8	399	2	Q64XP3_BACFR	Q5lgu1 bacteroides
423	85.5	4.9	426	2	Q5XNE5_9HEPC	Q5xne5 hepatitis c	496	84.5	4.8	426	2	Q5XN51_9HEPC	Q5xn51 hepatitis c
424	85.5	4.9	426	2	Q5XNE7_9HEPC	Q5xne7 hepatitis c	497	84.5	4.8	426	2	Q5XN58_9HEPC	Q5xn58 hepatitis c
425	85.5	4.9	436	1	FIBG_MOUSE	Q8vcm7 mus musculu	498	84.5	4.8	426	2	Q5XN67_9HEPC	Q5xn67 hepatitis c
426	85.5	4.9	468	1	AMYE_BACFI	P96513 bacillus fi	499	84.5	4.8	426	2	Q5XN69_9HEPC	Q5xn69 hepatitis c
427	85.5	4.9	476	2	Q4WJE2_ASPFU	Q4wje2 aspergillus	500	84.5	4.8	426	2	Q5XND6_9HEPC	Q5xnd6 hepatitis c
428	85.5	4.9	484	2	Q4SP25_TETNG	Q4sp25 tetraodon n	501	84.5	4.8	426	2	Q5XNG0_9HEPC	Q5xng0 hepatitis c
429	85.5	4.9	566	2	Q84110_9INFA	Q84110 influenza a	502	84.5	4.8	494	2	Q65G96_BACLD	Q65g96 bacillus li
430	85.5	4.9	566	2	Q84114_9INFA	Q84114 influenza a	503	84.5	4.8	499	2	Q6NW98_BRARE	Q6nw98 brachydanio
431	85.5	4.9	568	2	Q70J58_ASPFU	Q70j58 aspergillus	504	84.5	4.8	500	1	NIFD_RHICP	P06769 rhizobium s
432	85.5	4.9	594	2	Q4WQU0_ASPFU	Q4wqu0 aspergillus	505	84.5	4.8	543	2	Q7UGD7_RHOBA	Q7ugd7 rhodopirell
433	85.5	4.9	670	2	Q9EWU9_STRCO	Q9ewu9 streptomyc	506	84.5	4.8	566	2	Q918Q6_9INFA	Q918q6 influenza a
434	85.5	4.9	722	2	P96091_TREDE	P96091 treponema d	507	84.5	4.8	566	2	Q918Q8_9INFA	Q918q8 influenza a
435	85.5	4.9	804	2	O00089_ASPNG	O00089 aspergillus	508	84.5	4.8	610	1	CHIT_STRPL	P11220 streptomyc
436	85.5	4.9	804	2	O93933_ASPNG	O93933 aspergillus	509	84.5	4.8	725	2	Q5FAL3_NEIG1	Q5fal3 neisseria g
437	85.5	4.9	866	1	FIBA_HUMAN	P02671 homo sapien	510	84.5	4.8	739	2	Q9UWN2_9EURY	Q9uwn2 thermococcu
438	85.5	4.9	915	2	Q4QL82_HAEI8	Q4ql82 haemophilus	511	84.5	4.8	750	2	Q6D988_ERWCT	Q6d988 erwinia car
439	85.5	4.9	919	2	Q5SFH9_HAEIN	Q5sfh9 haemophilus	512	84.5	4.8	770	2	Q89LN9_BRAJA	Q89ln9 bradyrhizob
440	85.5	4.9	950	2	Q5DWB1_CLOPE	Q5dwb1 clostridium	513	84.5	4.8	848	2	Q91PK3_WSSV	Q91pk3 white spot
441	85.5	4.9	1358	1	TENR_HUMAN	Q92752 homo sapien	514	84.5	4.8	848	2	Q9QAL9_WSSV	Q9qal9 white spot
442	85.5	4.9	1806	1	COBAI_HUMAN	P12107 homo sapien	515	84.5	4.8	935	2	Q7XM01_ORYSA	Q7xm01 oryza sativ
443	85.5	4.9	1838	2	O88207_MOUSE	Q88207 mus musculu	516	84.5	4.8	939	2	Q7Q4V0_ANOGA	Q7q4v0 anopheles g
444	85.5	4.9	1840	2	Q60467_CRILO	Q60467 cricetulus	517	84.5	4.8	1077	2	Q977Q4_METMA	Q977q4 methanosarc
445	85.5	4.9	1840	2	Q9JI03_RAT	Q9ji03 rattus norv	518	84.5	4.8	1097	2	Q6C029_YARLI	Q6c029 yarrowia li
446	85.5	4.9	2475	2	Q501R6_XENTR	Q501r6 xenopus tro	519	84.5	4.8	1646	2	Q4PQT8_9HEPC	Q4pqt8 hepatitis c
447	85.5	4.9	2850	1	HORN_HUMAN	Q86yz3 homo sapien	520	84.5	4.8	1646	2	Q4PQT7_9HEPC	Q4pqt7 hepatitis c
448	85.5	4.9	2850	2	Q5UIF4_HUMAN	Q5ulf4 homo sapien	521	84.5	4.8	1835	2	Q9IAU4_CHICK	Q9iau4 gallus gall
449	85.5	4.9	2850	2	Q5DT20_HUMAN	Q5dt20 homo sapien	522	84.5	4.8	2076	2	Q7S7A9_NEUCR	Q7s7a9 neurospora
450	85	4.9	295	2	Q8H3E2_ORYSA	Q8h3e2 oryza sativ	523	84.5	4.8	2117	2	Q96U11_NEUCR	Q96u11 neurospora
451	85	4.9	303	2	Q5I041_XENLA	Q5i041 xenopus lae	524	84.5	4.8	2174	1	POLG_BOVEV	P12915 b genome po
452	85	4.9	314	2	Q5PRF5_XENLA	Q5prf5 xenopus lae	525	84.5	4.8	166	2	Q7QHK7_ANOGA	Q7qhk7 anopheles g
453	85	4.9	320	2	Q5AUM3_EMENI	Q5aum3 aspergillus	526	84	4.8	292	2	Q8T9V0_AEDAE	Q8t9v0 aedes aegypt
454	85	4.9	321	2	Q9HFS9_ASPAC	Q9hfs9 aspergillus	527	84	4.8	306	1	FCN2_MOUSE	Q70497 mus musculu
455	85	4.9	330	2	Q5TPG6_ANOGA	Q5tpg6 anopheles g	528	84	4.8	310	2	Q6PJ54_HUMAN	Q6pj54 homo sapien
456	85	4.9	331	2	Q87Q71_VIBPA	Q87q71 vibrio para	529	84	4.8	346	2	Q8PT18_METMA	Q8pt18 methanosarc
457	85	4.9	338	2	Q6DIT6_XENTR	Q6dit6 xenopus tro	530	84	4.8	364	2	Q8JIZ8_ORENI	Q8jiz8 magnaporthe
458	85	4.9	343	2	Q6DJE9_XENLA	Q6dje9 xenopus tro	531	84	4.8	420	1	PEL_BACSU	P39116 bacillus su
459	85	4.9	349	2	Q9HR20_HALSA	Q9hr20 halobacteri	532	84	4.8	420	2	Q6LEQ4_BACSP	Q6leq4 bacillus sp
460	85	4.9	356	2	Q95P98_HALRO	Q95p98 halocynthia	533	84	4.8	453	2	Q5XNJ7_9HEPC	Q5xnj7 hepatitis c
461	85	4.9	414	2	Q61KT2_CAEBR	Q61kt2 caenorhabdi	534	84	4.8	456	2	Q8XPK8_RALSO	Q8xpk8 ralstonia s
462	85	4.9	420	2	Q4IF74_GIBZE	Q4if74 gibberella	535	84	4.8	463	2	Q7JP70_CAEEL	Q7jp70 caenorhabdi
463	85	4.9	426	2	Q5XNK1_9HEPC	Q5xnk1 hepatitis c	536	84	4.8	465	2	Q18914_CAEEL	Q18914 caenorhabdi
464	85	4.9	430	2	Q4WD15_ASPFU	Q4wd15 aspergillus	537	84	4.8	510	2	Q4IFM2_GIBZE	Q4ifm2 gibberella
465	85	4.9	464	2	Q82LA2_STRAW	Q82la2 streptomyc	538	84	4.8	532	2	Q4IQ67_GIBZE	Q4iq67 gibberella
466	85	4.9	550	2	Q64MM2_BACFR	Q64mm2 bacteroides	539	84	4.8	551	1	AMT4_PSESA	P22963 pseudomonas
467	85	4.9	552	2	Q6DWT7_9INFA	Q6dwt7 influenza a	540	84	4.8				
468	85	4.9	554	2	Q5L7G1_BACFN	Q5l7g1 bacteroides	541	84	4.8				
469	85	4.9	556	2	Q6DXG9_9INFA	Q6dxg9 influenza a	542	84	4.8				

543	84	4.8	555	2	Q6B6R4_ORYSA	Q6b6r4	oryza sativ	616	83	4.8	240	2	Q61H40_CABER	Q61h40	caenorhabdi
544	84	4.8	565	2	Q82544_9INFA	Q82544	influenza a	617	83	4.8	254	2	Q5XK70_XENLA	Q5xk70	xenopus lae
545	84	4.8	586	1	INV3_ORYSA	Q56ud3	oryza sativ	618	83	4.8	317	2	Q5QTR2_HUMAN	Q5qtr2	homo sapien
546	84	4.8	587	2	Q96459_STRPU	Q96459	strongyloce	619	83	4.8	319	2	Q5FW10_XENTR	Q5fw10	xenopus tro
547	84	4.8	638	2	Q9VNX8_DROME	Q9vnx8	drosophila	620	83	4.8	363	2	O45822_CABEL	O45822	caenorhabdi
548	84	4.8	684	2	Q6DHS2_BRARE	Q6dhs2	brachydanio	621	83	4.8	367	2	Q70EW4_HOMGA	Q70ew4	hohmarus gam
549	84	4.8	782	1	FIBA_RAT	P06399	rattus norv	622	83	4.8	371	2	Q5MIY7_AEDAL	Q5miy7	aedes albop
550	84	4.8	782	2	Q7TQ70_RAT	Q7tq70	rattus norv	623	83	4.8	401	2	Q9SUT6_BIOGL	Q9sut6	biomphalari
551	84	4.8	836	1	PAPC_ECOLI	P07110	escherichia	624	83	4.8	407	2	Q9PU54_CHICK	Q9pu54	gallus gall
552	84	4.8	836	2	Q8GA01_ECOLI	Q8ga01	escherichia	625	83	4.8	413	2	Q84592_STRAU	Q845a2	streptomyce
553	84	4.8	839	2	Q4PBG3_ECOLI	Q4fbg3	escherichia	626	83	4.8	426	2	Q5XNJ6_9HEPC	Q5xnj6	hepatitis c
554	83.5	4.8	257	1	MFAP4_MOUSE	Q9dlh9	mus musculu	627	83	4.8	432	2	Q7UUR7_RHOBA	Q7uur7	rhodopirell
555	83.5	4.8	266	2	Q7QGR8_ANOGA	Q7qgr8	anopheles g	628	83	4.8	459	2	Q7Z7X3_TRIVI	Q7z7x3	trichoderma
556	83.5	4.8	268	2	Q6VPN2_ANOGA	Q6vpn2	anopheles g	629	83	4.8	493	2	Q6QHT4_BACCI	Q6ght4	bacillus ci
557	83.5	4.8	268	2	Q6VPN3_ANOGA	Q6vpn3	anopheles g	630	83	4.8	501	1	HDAC_ARATH	O22446	arabidopsis
558	83.5	4.8	279	2	Q7ZT73_XENLA	Q7zt73	xenopus lae	631	83	4.8	507	2	Q6QDD6_9RHAB	Q6gdd6	viral hemor
559	83.5	4.8	308	2	Q17452_CABEL	Q17452	caenorhabdi	632	83	4.8	516	2	Q9LHQ8_ARATH	Q9lqh8	arabidopsis
560	83.5	4.8	337	1	ANGL7_MOUSE	Q8rlq3	mus musculu	633	83	4.8	523	2	Q742T0_MYCPA	Q742t0	mycobacteri
561	83.5	4.8	354	2	Q9U6I1_DROAN	Q9u6i1	drosophila	634	83	4.8	543	2	Q7QHL5_ANOGA	Q7qhl5	anopheles g
562	83.5	4.8	359	2	Q8I188_DROVI	Q8i188	drosophila	635	83	4.8	553	1	VH65_NPVAC	Q08539	autographa
563	83.5	4.8	392	2	Q39171_9INFA	Q39171	influenza a	636	83	4.8	564	2	Q84W45_ARATH	Q84w45	arabidopsis
564	83.5	4.8	426	2	Q5XML9_9HEPC	Q5xml9	hepatitis c	637	83	4.8	568	2	Q7Z4E9_HUMAN	Q7z4e9	homo sapien
565	83.5	4.8	426	2	Q5XMU0_9HEPC	Q5xmu0	hepatitis c	638	83	4.8	585	2	Q96EW9_HUMAN	Q96ew9	homo sapien
566	83.5	4.8	426	2	Q5XMU1_9HEPC	Q5xmu1	hepatitis c	639	83	4.8	585	2	Q96K81_HUMAN	Q96k81	homo sapien
567	83.5	4.8	426	2	Q5XMU3_9HEPC	Q5xmu3	hepatitis c	640	83	4.8	609	2	Q9BY44_HUMAN	Q9by44	homo sapien
568	83.5	4.8	426	2	Q5XN21_9HEPC	Q5xn21	hepatitis c	641	83	4.8	730	2	Q8DS80_STRMU	Q8ds80	streptococc
569	83.5	4.8	426	2	Q5XN65_9HEPC	Q5xn65	hepatitis c	642	83	4.8	737	2	Q8T316_PARLI	Q8t316	paracentrot
570	83.5	4.8	426	2	Q5XN70_9HEPC	Q5xn70	hepatitis c	643	83	4.8	760	2	Q8EA47_SHEON	Q8ea47	shewanella
571	83.5	4.8	426	2	Q5XN75_9HEPC	Q5xn75	hepatitis c	644	83	4.8	796	2	Q8ZRS1_SALTY	Q8zrs1	salmonella
572	83.5	4.8	426	2	Q5XN98_9HEPC	Q5xn98	hepatitis c	645	83	4.8	802	2	Q57T86_SALCH	Q57t86	salmonella
573	83.5	4.8	426	2	Q5XND8_9HEPC	Q5xnd8	hepatitis c	646	83	4.8	904	2	Q82NR8_STRAW	Q82nr8	streptomyce
574	83.5	4.8	426	2	Q5XNB1_9HEPC	Q5xne1	hepatitis c	647	83	4.8	914	2	Q9IF30_ADEBA	Q9if30	bovine aden
575	83.5	4.8	430	2	Q98N05_RHILO	Q98n05	rhizobium l	648	83	4.8	977	2	Q4UNB6_RICPE	Q4unb6	rickettsia
576	83.5	4.8	441	2	O13337_MAGGR	O13337	magnaporthe	649	83	4.8	993	2	Q5LHN8_BACFN	Q5lhn8	bacteroides
577	83.5	4.8	451	2	Q8H788_ARATH	Q8h788	arabidopsis	650	83	4.8	1103	2	Q6MZP4_HUMAN	Q6mzf4	homo sapien
578	83.5	4.8	467	2	Q86WX2_HUMAN	Q86wx2	homo sapien	651	83	4.8	1309	2	O64428_CHLVU	O64428	chlorella v
579	83.5	4.8	467	2	Q8RWX7_ARATH	Q8rwx7	arabidopsis	652	83	4.8	1644	2	Q4PQQ7_9HEPC	Q4pqq7	hepatitis c
580	83.5	4.8	476	2	Q8T5Y9_HUMAN	Q8t5y9	homo sapien	653	83	4.8	2019	2	Q80YX2_MOUSE	Q80yx2	mus musculu
581	83.5	4.8	489	2	Q90Z18_BRARE	Q90z18	brachydanio	654	83	4.8	2019	2	Q64706_MOUSE	Q64706	mus musculu
582	83.5	4.8	500	1	NIFD_BRASP	P06120	bradyrhizob	655	83	4.8	2110	2	Q80YX1_MOUSE	Q80yx1	mus musculu
583	83.5	4.8	543	2	Q7PC52_9ALTE	Q7pc52	saccharopha	656	83	4.8	2193	2	Q6MZM7_HUMAN	Q6mzm7	homo sapien
584	83.5	4.8	566	2	Q82545_9INFA	Q82545	influenza a	657	83	4.8	2217	2	Q585T2_HUMAN	Q585t2	homo sapien
585	83.5	4.8	566	2	Q82751_9ORTO	Q82751	unidentifie	658	83	4.8	2240	2	Q68DP8_HUMAN	Q68dp8	homo sapien
586	83.5	4.8	566	2	Q918Q7_9INFA	Q918q7	influenza a	659	83	4.8	2265	2	Q60FE4_HUMAN	Q60fe4	homo sapien
587	83.5	4.8	576	2	Q4KP40_9HEPC	Q4kp40	hepatitis c	660	83	4.8	2267	2	Q68DP9_HUMAN	Q68dp9	homo sapien
588	83.5	4.8	601	2	Q5ZMM1_CHICK	Q5zmm1	gallus gall	661	83	4.8	2296	2	Q6N0A6_HUMAN	Q6n0a6	homo sapien
589	83.5	4.8	608	2	Q82P56_STRAW	Q82p56	streptomyce	662	83	4.8	2351	2	Q59EH1_HUMAN	Q59eh1	homo sapien
590	83.5	4.8	613	2	Q4TSH2_TETNG	Q4tsh2	tetraodon n	663	83	4.8	2357	2	Q68DT4_HUMAN	Q68dt4	homo sapien
591	83.5	4.8	688	2	Q9SHY2_ARATH	Q9shy2	arabidopsis	664	83	4.8	2386	1	FINC_HUMAN	P02751	homo sapien
592	83.5	4.8	698	2	Q83LL6_SHIFL	Q83ll6	shigella fl	665	83	4.8	2444	2	Q6N025_HUMAN	Q6n025	homo sapien
593	83.5	4.8	702	2	Q32747_9POAL	Q32747	oryzopsis r	666	83	4.8	2477	2	Q6MZU5_HUMAN	Q6mzu5	homo sapien
594	83.5	4.8	725	2	O52158_NEIME	O52158	neisseria m	667	83	4.8	3010	2	Q5R2D7_9HEPC	Q5r2d7	hepatitis c
595	83.5	4.8	764	2	Q8PH33_XANAC	Q8ph33	xanthomonas	668	82.5	4.7	226	2	Q4RDUI_TETNG	Q4rdul	tetraodon n
596	83.5	4.8	796	2	Q5PDA4_SALPA	Q5pda4	salmonella	669	82.5	4.7	246	2	Q8I6X2_9TREM	Q8i6x2	opisthorchi
597	83.5	4.8	870	2	Q4UTW2_XANCP	Q4utw2	xanthomonas	670	82.5	4.7	307	2	Q5ZR75_CABEL	Q5zr75	caenorhabdi
598	83.5	4.8	870	2	Q8P9S3_XANCP	Q8p9s3	xanthomonas	671	82.5	4.7	312	1	FGL1_HUMAN	Q08830	homo sapien
599	83.5	4.8	1017	2	Q59HB5_HUMAN	Q59hb5	homo sapien	672	82.5	4.7	312	2	Q8NG32_HUMAN	Q8ng32	homo sapien
600	83.5	4.8	1053	2	Q4RHV2_TETNG	Q4rhv2	tetraodon n	673	82.5	4.7	312	2	Q53YF1_HUMAN	Q53yfl	homo sapien
601	83.5	4.8	1109	2	Q64VL9_BACFR	Q64vl9	bacteroides	674	82.5	4.7	312	2	Q4PUH9_HUMAN	Q4pjh9	homo sapien
602	83.5	4.8	1233	2	Q6ZSN4_HUMAN	Q6zsn4	homo sapien	675	82.5	4.7	388	1	ANGL5_HUMAN	Q86xs5	homo sapien
603	83.5	4.8	1379	2	Q6T256_HUMAN	Q6t256	homo sapien	676	82.5	4.7	405	1	CLR6_SCHPO	O59702	schizosacch
604	83.5	4.8	1588	2	Q8XXK8_CLOPE	Q8xxk8	clostridium	677	82.5	4.7	426	2	Q5XMM3_9HEPC	Q5xmm3	hepatitis c
605	83.5	4.8	1644	2	Q4PQT4_9HEPC	Q4pqt4	hepatitis c	678	82.5	4.7	426	2	Q5XN53_9HEPC	Q5xn53	hepatitis c
606	83.5	4.8	1644	2	Q4PQT3_9HEPC	Q4pqt3	hepatitis c	679	82.5	4.7	426	2	Q5XN74_9HEPC	Q5xn74	hepatitis c
607	83.5	4.8	1644	2	Q4PQT2_9HEPC	Q4pqt2	hepatitis c	680	82.5	4.7	455	2	Q9SHG2_ARATH	Q9shg2	arabidopsis
608	83.5	4.8	1806	2	Q5VT31_HUMAN	Q5vt31	homo sapien	681	82.5	4.7	460	2	Q82AS5_STRAW	Q82as5	streptomyce
609	83.5	4.8	2391	2	Q7XR12_ORYSA	Q7xrl2	oryza sativ	682	82.5	4.7	488	2	Q4QC5_TETNG	Q4rqc5	tetraodon n
610	83.5	4.8	3411	2	Q6PX46_9FLAV	Q6px46	yellow feve	683	82.5	4.7	489	2	Q6GP67_XENLA	Q6gp67	xenopus lae
611	83.5	4.8	3411	2	Q6J3P1_9FLAV	Q6j3p1	yellow feve	684	82.5	4.7	502	2	Q8GWU4_ARATH	Q8gwu4	arabidopsis
612	83.5	4.8	3471	2	Q6HBX5_BACHK	Q6hbx5	bacillus th	685	82.5	4.7	564	2	Q8ZNS2_SALTY	Q8zn82	salmonella
613	83.5	4.8	4163	2	Q9LAE6_RHILT	Q9lae6	rhizobium l	686	82.5	4.7	576	2	Q4KP48_9HEPC	Q4kp48	hepatitis c
614	83.5	4.8	5839	2	Q5RGP8_BRARE	Q5rgp8	brachydanio	687	82.5	4.7	587	2	Q8VR37_ECOLI	Q8vr37	escherichia
615	83	4.8	169	2	Q868G5_9ACAR	Q868g5	amblyomma a	688	82.5	4.7	591	2	Q96HC0_HUMAN	Q96hc0	homo sapien

689	82.5	4.7	609	1	INV_KLUJLA	Q9Y746 kluyveromyc	762	82	4.7	7716	2	Q7UWZ8_RHOBA	Q7uwz8 rhodopirell
690	82.5	4.7	609	2	Q9Z9M8_STRCO	Q9zm8 streptomyce	763	81.5	4.7	255	1	MFAP4_HUMAN	P55083 homo sapien
691	82.5	4.7	611	2	Q4H3J2_CIOIN	Q4hj2 ciona intes	764	81.5	4.7	268	2	Q988B9_RHILO	Q988b9 rhizobium l
692	82.5	4.7	621	2	Q9F486_ALTSO	Q9f486 alteromonas	765	81.5	4.7	280	2	Q6K3N4_ORYSA	Q6k3n4 oryza sativ
693	82.5	4.7	621	2	Q53401_9ALTE	Q53401 alteromonas	766	81.5	4.7	313	2	Q6GLL5_XENLA	Q6gl15 xenopus lae
694	82.5	4.7	629	2	Q82M60_STRAW	Q82m60 streptomyce	767	81.5	4.7	319	1	FCN2_RAT	P57756 rattus norv
695	82.5	4.7	645	2	Q57M24_SALCH	Q57m24 salmonella	768	81.5	4.7	321	2	Q7SYN8_XENLA	P77575 xenopus lae
696	82.5	4.7	646	2	Q7PP64_ANOGA	Q7pp64 anopheles g	769	81.5	4.7	326	2	Q98UT8_9HEPC	Q98ut8 hepatitis c
697	82.5	4.7	652	1	AORSN_ASPOR	Q8nk92 aspergillus	770	81.5	4.7	326	2	Q98UT9_9HEPC	Q98ut9 hepatitis c
698	82.5	4.7	660	2	Q87QD1_VIBPA	Q87qd1 vibrio para	771	81.5	4.7	326	2	Q98UUI_9HEPC	Q98uui hepatitis c
699	82.5	4.7	669	2	Q584L1_9TRYP	Q584l1 trypanosoma	772	81.5	4.7	341	2	Q966W1_HALRO	Q966w1 halocynthia
700	82.5	4.7	698	2	Q7AFW2_ECO57	Q7afw2 escherichia	773	81.5	4.7	349	2	Q4WGN5_ASPFU	Q4wgn5 aspergillus
701	82.5	4.7	749	2	Q9YGE8_ONCMY	Q8x542 escherichia	774	81.5	4.7	363	2	Q8TA02_9TRYP	Q8ta02 trypanosoma
702	82.5	4.7	798	2	Q9A3Q5_CAUCR	Q9yge8 oncorhynchu	775	81.5	4.7	426	2	Q5XNB5_9HEPC	Q5xne6 hepatitis c
703	82.5	4.7	840	2	Q7QYW9_GIALA	Q9a3q5 caulobacter	776	81.5	4.7	444	2	Q8VT32_ENTFA	Q8vt32 enterococcu
704	82.5	4.7	942	2	TARP2_CHLTR	Q7qyw9 giardia lam	777	81.5	4.7	446	2	Q9F1I3_ENTFA	Q9f1i3 enterococcu
705	82.5	4.7	1005	1	Q9HVM8_PSEAE	Q6gx35 chlamydia t	778	81.5	4.7	488	2	Q9I589_XENLA	Q9i589 xenopus lae
706	82.5	4.7	1161	2	Q9HVM8_PSEAE	Q9hvm8 pseudomonas	779	81.5	4.7	514	1	AMY_BACAM	P00692 bacillus am
707	82.5	4.7	1226	1	MIB_DROME	Q9vux2 drosophila	780	81.5	4.7	535	2	Q9KVI8_VIBCH	Q9kvi8 vibrio chol
708	82.5	4.7	1254	1	POL5_EEVM	P36331 venezuelan	781	81.5	4.7	553	2	Q4HWK2_GIBZE	Q4hwk2 gibberella
709	82.5	4.7	1254	1	Q9WC26_9VIRU	Q9wc26 venezuelan	782	81.5	4.7	559	2	Q8A0A2_BACTN	Q8a0a2 bacteroides
710	82.5	4.7	1644	2	Q4PQS6_9HEPC	Q4pqs6 hepatitis c	783	81.5	4.7	566	2	Q9YTB8_9INFA	Q9ytb8 influenza a
711	82.5	4.7	1792	2	Q59EE7_HUMAN	Q59ee7 homo sapien	784	81.5	4.7	607	2	Q6ND92_RHOPA	Q6nd92 rhodopseudo
712	82.5	4.7	1838	1	CO5A1_HUMAN	P20908 homo sapien	785	81.5	4.7	657	2	Q564H7_HUMAN	Q564h7 homo sapien
713	82.5	4.7	1838	2	Q5SUX4_HUMAN	Q5sux4 homo sapien	786	81.5	4.7	673	2	Q8N4R1_HUMAN	Q8n4r1 homo sapien
714	82.5	4.7	1843	2	Q9GQS2_LEITR	Q9gqs2 leishmania	787	81.5	4.7	675	2	Q5ST46_HUMAN	Q5st46 homo sapien
715	82.5	4.7	4135	2	O18977_BOVIN	O18977 bos taurus	788	81.5	4.7	675	2	Q8PSX7_METMA	Q8pax7 methanosarc
716	82	4.7	220	2	Q02411_PIG	Q02411 sus scrofa	789	81.5	4.7	681	2	Q83WH1_STRGR	Q83wh1 streptomyce
717	82	4.7	274	2	Q5TVE0_ANOGA	Q5tve0 anopheles g	790	81.5	4.7	719	2	P72539_STRPR	P72539 streptomyce
718	82	4.7	279	2	Q5YD75_LOXRE	Q5yd75 loxosceles	791	81.5	4.7	725	2	Q4LDN7_NEIME	Q4ldn7 neisseria m
719	82	4.7	340	2	Q58LR7_9CAUD	Q58lr7 cyranophage	792	81.5	4.7	749	2	Q8VWM3_WHEAT	Q8vwm3 triticum ae
720	82	4.7	360	2	Q9F889_SALTI	Q9f889 salmonella	793	81.5	4.7	785	2	O8VWM3_WHEAT	Q7z391 homo sapien
721	82	4.7	363	1	OMPF_SALTY	Q561i3 salmonella	794	81.5	4.7	789	1	ADAM1_RAT	Q8vwm3 triticum ae
722	82	4.7	363	1	OMPF_SALTY	P37432 salmonella	795	81.5	4.7	789	2	Q66HK9_RAT	P70505 rattus norv
723	82	4.7	363	2	Q4Z5H7_PLABE	Q4z5h7 plasmodium	796	81.5	4.7	795	2	Q9KEL0_BACHD	Q66hk9 rattus norv
724	82	4.7	363	2	Q9K3E7_SALET	Q9k3e7 salmonella	797	81.5	4.7	795	2	Q59GU7_HUMAN	Q9kel0 bacillus ha
725	82	4.7	363	2	Q5PGE9_SALPA	Q5pge9 salmonella	798	81.5	4.7	884	2	O87343_NEIME	Q59gu7 homo sapien
726	82	4.7	365	2	Q57QZ9_SALCH	Q57qz9 salmonella	799	81.5	4.7	943	2	O87343_NEIME	O87343 neisseria m
727	82	4.7	370	1	GLNA_DEBHA	Q6b4u7 debaryomyce	800	81.5	4.7	1008	2	Q8X2I3_TALEM	Q8x2i3 talaromyces
728	82	4.7	373	1	GLNA_CHICK	P16580 gallus gall	801	81.5	4.7	1017	1	DPOL_ADEB2	Q72539 bovine aden
729	82	4.7	391	2	Q7U504_SYNPX	Q7u504 synchococc	802	81.5	4.7	1037	2	Q8EJ34_SHEON	Q8ej34 shewanella
730	82	4.7	417	2	Q29038_PIG	Q29038 sus scrofa	803	81.5	4.7	1103	2	Q7Y4Q8_BPR69	Q7y4q8 bacterioph
731	82	4.7	426	2	Q5XNK0_9HEPC	Q5xnk0 hepatitis c	804	81.5	4.7	1134	2	Q7M6F2_ADEB2	Q7m6f2 bovine aden
732	82	4.7	463	1	GUN1_TRILO	Q12714 trichoderma	805	81.5	4.7	1395	2	Q4SHU0_TETNG	Q4shu0 tetraodon n
733	82	4.7	466	2	Q4UAT5_THBAN	Q4uat5 theileria a	806	81.5	4.7	1644	2	Q4PQV0_9HEPC	Q4pqv0 hepatitis c
734	82	4.7	497	2	Q628S4_CAEBR	Q628s4 caenorhabdi	807	81.5	4.7	1644	2	Q4PQT6_9HEPC	Q4pqt6 hepatitis c
735	82	4.7	500	2	Q9LKG1_MESCR	Q9lkg1 mesembryant	808	81.5	4.7	1644	2	Q4PQT5_9HEPC	Q4pqt5 hepatitis c
736	82	4.7	501	2	Q73EX0_BACCI	Q73ex0 bacillus ce	809	81.5	4.7	1646	2	Q4PQT0_9HEPC	Q4pqt0 hepatitis c
737	82	4.7	507	2	Q6QDD4_9RHAB	Q6qdd4 viral hemor	810	81.5	4.7	1646	2	Q4PQT9_9HEPC	Q4pqt9 hepatitis c
738	82	4.7	507	2	Q6QDE8_9RHAB	Q6qde8 viral hemor	811	81.5	4.7	1835	2	Q6MD86_PAROW	Q6md86 parachlamyd
739	82	4.7	507	2	Q6QDI4_9RHAB	Q6qdi4 viral hemor	812	81.5	4.7	2079	2	Q7UF08_RHOBA	Q7uf08 rhodopirell
740	82	4.7	557	2	Q6DWU5_9INFA	Q6dws5 influenza a	813	81.5	4.7	2120	2	Q5DM98_9VIRU	Q5dm98 taura syndr
741	82	4.7	572	2	O16778_CABEL	O16778 caenorhabdi	814	81.5	4.7	2477	1	FINC_RAT	P04937 rattus norv
742	82	4.7	590	2	Q9R9S7_AERPUP	Q9r9s7 aeromonas p	815	81.5	4.7	3295	2	Q5JNX3_HUMAN	Q5jnx3 homo sapien
743	82	4.7	593	1	PDC1_PEA	P51850 pisum sativ	816	81.5	4.7	3494	2	Q7LC53_HUMAN	Q7lc53 homo sapien
744	82	4.7	607	2	Q96536_ARATH	Q96536 arabidopsis	817	81.5	4.7	3623	2	O60494_HUMAN	O60494 homo sapien
745	82	4.7	634	1	DHSX_YEAST	P47052 saccharomyc	818	81.5	4.7	3623	2	Q5VTA6_HUMAN	Q5vta6 homo sapien
746	82	4.7	652	1	SSP1_SCHPO	P50526 schizosacch	819	81.5	4.7	4222	2	Q5ST74_HUMAN	Q5st74 homo sapien
747	82	4.7	658	2	O652I4_VOLCA	O652i4 volvox cart	820	81.5	4.7	4222	2	Q5SQD3_HUMAN	Q5sqd3 homo sapien
748	82	4.7	663	2	P91100_CABEL	P91100 caenorhabdi	821	81.5	4.7	4288	2	Q9NPK9_HUMAN	Q9npk9 homo sapien
749	82	4.7	702	2	Q32334_9POAL	Q32334 guadua pani	822	81.5	4.7	4289	1	TENX_HUMAN	P22105 homo sapien
750	82	4.7	715	2	Q5YT39_NOCFA	Q5yt39 nocardia fa	823	81.5	4.7	4345	2	Q9VLA0_DROSOPHILA	Q9vla0 drosophila
751	82	4.7	716	2	Q82TZ3_NITEU	Q82tz3 nitrosomona	824	81.5	4.7	4374	2	Q7KTG2_DROME	Q7ktg2 drosophila
752	82	4.7	732	2	O48899_MAIZE	O48899 zea mays (m	825	81	4.6	163	2	Q4ISH5_GIBZE	Q4ish5 gibberella
753	82	4.7	793	2	Q84YG7_SOLTU	Q84yg7 solanum tub	826	81	4.6	198	2	Q96SJ7_HUMAN	Q96sj7 homo sapien
754	82	4.7	865	2	Q7EZ33_ORYSA	Q7ez33 oryza sativ	827	81	4.6	200	2	Q8BMV1_MOUSE	Q8bm1 mus musculu
755	82	4.7	1051	2	Q5LAH9_BACFN	Q5lah9 bacteroides	828	81	4.6	212	2	Q9SM49_SACOF	Q9sm49 saccharum o
756	82	4.7	1051	2	Q64QW8_BACFR	Q64qw8 bacteroides	829	81	4.6	273	2	Q4HH38_CAMCO	Q4hh38 campylobact
757	82	4.7	1123	2	Q4N6B2_THEPA	Q4n6b2 theileria p	830	81	4.6	303	2	Q8GV32_ORYSA	Q8gv32 oryza sativ
758	82	4.7	1150	2	Q7EYB2_ORYSA	Q7eye2 oryza sativ	831	81	4.6	333	2	Q9Y892_COLGL	Q9y892 colletotric
759	82	4.7	1265	2	Q60BT5_METCA	Q60bt5 methylococc	832	81	4.6	344	2	Q9JFV8_9INFA	Q9jfv8 influenza a
760	82	4.7	1389	2	Q4REV4_TETNG	Q4rev4 tetraodon n	833	81	4.6	378	1	VE2_HPV30	P36790 human papil
761	82	4.7	3010	1	POLG_HCVH	P27958 h genome po	834	81	4.6	379	2	Q75FZ6_LEPIC	Q75fz6 leptospira



835	81	4.6	404	2	Q4RXV0_TETNG	Q4rxv0 tetraodon n
836	81	4.6	432	1	FGL2_MOUSE	p12804 mus musculus
837	81	4.6	432	2	Q54K3_MOUSE	Q544k3 mus musculus
838	81	4.6	445	2	Q5G3N2_ENTFA	Q5g3n2 enterococcu
839	81	4.6	447	2	Q82YL0_ENTFA	Q82yl0 enterococcu
840	81	4.6	507	2	Q6QDE6_9RHAB	Q6qde6 viral hemor
841	81	4.6	513	2	Q90Z19_BRARE	Q90z19 brachydanio
842	81	4.6	518	2	Q5LH40_BACFN	Q5lh40 bacterioides
843	81	4.6	518	2	Q64XZ7_BACFR	Q64xz7 bacterioides
844	81	4.6	528	2	Q13344_HUMAN	Q13344 homo sapien
845	81	4.6	548	1	AMT4_PSEST	p13507 pseudomonas
846	81	4.6	576	2	Q7VV16_BORPE	Q7vv16 bordetella
847	81	4.6	603	2	Q9M040_ARATH	Q9m040 arabidopsis
848	81	4.6	605	2	Q8T5Z5_TRISP	Q8t5z5 trichinella
849	81	4.6	668	2	Q8K0W0_MOUSE	Q8k0w0 mus musculus
850	81	4.6	691	2	Q6AZ11_XENLA	Q6az11 xenopus lae
851	81	4.6	726	2	Q6V7U2_9VIRU	Q6v7u2 snake parvo
852	81	4.6	767	2	Q9QUD8_9VIRU	Q9qud8 torque teno
853	81	4.6	792	1	OSTA_XYLFA	Q9pf41 xylella fas
854	81	4.6	792	1	OSTA_XYLPF	Q87ai9 xylella fas
855	81	4.6	817	2	P73619_SYNY3	P73619 synechocyst
856	81	4.6	872	2	Q9RY85_DEIRA	Q9ry85 deinococcus
857	81	4.6	873	2	Q5YZV6_NOCFA	Q5yzv6 nocardia fa
858	81	4.6	890	2	O86727_STRCO	O86727 streptomyce
859	81	4.6	902	1	FTHFD_HUMAN	Q75891 homo sapien
860	81	4.6	902	2	Q53H87_HUMAN	Q53h87 homo sapien
861	81	4.6	940	2	Q8Y4N9_LISMO	Q8y4n9 listeria mo
862	81	4.6	954	2	Q59G10_HUMAN	Q59g10 homo sapien
863	81	4.6	1028	2	O68083_RHOCA	O68083 rhodobacter
864	81	4.6	1082	2	Q6N3Z4_RHOPA	Q6n3z4 rhodopseudo
865	81	4.6	1349	2	Q6CW00_KJULA	Q6cw00 kluyveromyc
866	81	4.6	1628	2	Q6C1S4_YARLI	Q6c1s4 yarrowia li
867	81	4.6	1785	2	Q9Y4V9_HUMAN	Q9y4v9 homo sapien
868	81	4.6	1785	2	Q5JR23_HUMAN	Q5jr23 homo sapien
869	81	4.6	1785	2	Q9Y211_HUMAN	Q9y211 homo sapien
870	81	4.6	1819	2	Q4TT23_9SPHN	Q4tt23 erythrobact
871	81	4.6	2403	2	Q9UGM2_HUMAN	Q9ugm2 homo sapien
872	81	4.6	2403	2	Q5JR22_HUMAN	Q5jr22 homo sapien
873	81	4.6	2413	2	Q9UKJ4_HUMAN	Q9ukj4 homo sapien
874	81	4.6	2413	2	Q96DU4_HUMAN	Q96du4 homo sapien
875	81	4.6	2413	2	Q5JR26_HUMAN	Q5jr26 homo sapien
876	81	4.6	2426	2	Q9UGM3_HUMAN	Q9ugm3 homo sapien
877	81	4.6	2542	2	Q5JR25_HUMAN	Q5jr25 homo sapien
878	81	4.6	3670	1	CSMD3_HUMAN	Q7z407 homo sapien
879	80.5	4.6	140	2	Q50FT9_CAMJE	Q50ft9 campylobact
880	80.5	4.6	164	2	Q855P8_9CAUD	Q855p8 mycobacteri
881	80.5	4.6	180	2	Q7Q214_ANOGA	Q7q214 anopheles g
882	80.5	4.6	211	2	Q7QHK4_PLAYO	Q7qhk4 anopheles g
883	80.5	4.6	220	2	Q7R7G6_PLAYO	Q7r7g6 plasmodium
884	80.5	4.6	223	2	Q5BLF1_BRARE	Q5blf1 brachydanio
885	80.5	4.6	293	2	Q5DIX9_SCHJA	Q5dix9 schistosoma
886	80.5	4.6	300	2	Q8VD40_CAVPO	Q8vd40 cavia porce
887	80.5	4.6	315	2	Q98UL0_9HEPC	Q98ul0 hepatitis c
888	80.5	4.6	319	2	O431015_SCHPO	Q43015 schizosacch
889	80.5	4.6	334	2	O62135_CAEEL	O62135 caenorhabdi
890	80.5	4.6	342	2	Q9TXW7_CABEL	Q9txw7 caenorhabdi
891	80.5	4.6	343	2	Q9JFV5_9INFA	Q9jfv5 influenza a
892	80.5	4.6	371	2	Q63LN4_BURPS	Q63ln4 burkholderi
893	80.5	4.6	371	2	Q62BQ4_BURMA	Q62bq4 burkholderi
894	80.5	4.6	398	2	Q8A095_BACTN	Q8a095 bacterioides
895	80.5	4.6	406	2	Q9S4K6_ECOLI	Q9s4k6 escherichia
896	80.5	4.6	418	2	Q95L38_BOVIN	Q95l38 bos taurus
897	80.5	4.6	421	2	Q4TC97_TETNG	Q4tc97 tetraodon n
898	80.5	4.6	425	2	Q9JPP7_NEIME	Q9jpp7 neisseria m
899	80.5	4.6	426	2	Q5XML8_9HEPC	Q5xml8 hepatitis c
900	80.5	4.6	426	2	Q5XMM0_9HEPC	Q5xmm0 hepatitis c
901	80.5	4.6	426	2	Q5XMM8_9HEPC	Q5xmm8 hepatitis c
902	80.5	4.6	426	2	Q5XMM8_9HEPC	Q5xmm8 hepatitis c
903	80.5	4.6	426	2	Q5XMMX3_9HEPC	Q5xmx3 hepatitis c
904	80.5	4.6	426	2	Q5XN64_9HEPC	Q5xn64 hepatitis c
905	80.5	4.6	426	2	Q5XN77_9HEPC	Q5xn77 hepatitis c
906	80.5	4.6	426	2	Q5XNC5_9HEPC	Q5xnc5 hepatitis c
907	80.5	4.6	426	2	Q5XNC9_9HEPC	Q5xnc9 hepatitis c

908	80.5	4.6	455	1	ANGL3_MOUSE	Q9r182 mus musculu
909	80.5	4.6	473	2	O70605_RAT	O70605 rattus norv
910	80.5	4.6	548	1	THER_BACST	P06874 bacillus st
911	80.5	4.6	576	2	Q4KP36_9HEPC	Q4kp36 hepatitis c
912	80.5	4.6	576	2	Q4KP37_9HEPC	Q4kp37 hepatitis c
913	80.5	4.6	576	2	Q4KP38_9HEPC	Q4kp38 hepatitis c
914	80.5	4.6	576	2	Q4KP39_9HEPC	Q4kp39 hepatitis c
915	80.5	4.6	576	2	Q4KP45_9HEPC	Q4kp45 hepatitis c
916	80.5	4.6	629	2	Q4HU61_GIBZE	Q4hu61 gibberella
917	80.5	4.6	728	2	Q7QBP4_ANOGA	Q7qbp4 anopheles g
918	80.5	4.6	733	2	Q8EDM8_SHEON	Q8edm8 shewanella
919	80.5	4.6	748	2	Q4HXL9_GIBZE	Q4hxl9 gibberella
920	80.5	4.6	778	2	Q04184_9HEPC	Q04184 hepatitis c
921	80.5	4.6	803	2	Q934J0_9BACL	Q934j0 paenibacill
922	80.5	4.6	815	2	Q80B16_9HEPC	Q80b16 hepatitis c
923	80.5	4.6	841	2	Q9ZJ88_HELPJ	Q9zj88 helicobacte
924	80.5	4.6	867	1	SFMD_ECOLI	P77468 escherichia
925	80.5	4.6	869	2	Q7AGT8_ECO57	Q7agt8 escherichia
926	80.5	4.6	869	2	Q8XCT4_ECO57	Q8xct4 escherichia
927	80.5	4.6	889	2	Q6XLI6_FUGRU	Q6xli6 fugu rubrip
928	80.5	4.6	921	2	Q6CFI8_YARLI	Q6cfi8 yarrowia li
929	80.5	4.6	955	2	Q21750_CAEEL	Q21750 caenorhabdi
930	80.5	4.6	994	1	EPHB2_MOUSE	P54763 mus musculu
931	80.5	4.6	998	2	Q9HLQ9_THEAC	Q9hlq9 thermoplasm
932	80.5	4.6	1001	2	Q58M71_9CAUD	Q58m71 cyanophage
933	80.5	4.6	1021	2	Q6GTQ7_MOUSE	Q6gtq7 mus musculu
934	80.5	4.6	1029	2	Q6P5F1_MOUSE	Q6p5f1 mus musculu
935	80.5	4.6	1100	2	Q8A2Y1_BACTN	Q8a2y1 bacteroides
936	80.5	4.6	1254	2	Q8V291_9VIRU	Q8v291 venezuelan
937	80.5	4.6	1254	2	Q88979_9VIRU	Q88979 venezuelan
938	80.5	4.6	1254	2	Q8V293_9VIRU	Q8v293 venezuelan
939	80.5	4.6	1254	2	Q9YKD3_9VIRU	Q9ykd3 venezuelan
940	80.5	4.6	1254	2	Q5IBC2_9VIRU	Q5ibc2 venezuelan
941	80.5	4.6	1264	2	Q8UYH1_9VIRU	Q8uyh1 venezuelan
942	80.5	4.6	1480	2	Q5B7I5_EMENI	Q5b7i5 aspergillus
943	80.5	4.6	1644	2	Q4PQU7_9HEPC	Q4pqu7 hepatitis c
944	80.5	4.6	1644	2	Q4PQS8_9HEPC	Q4pq8 hepatitis c
945	80.5	4.6	1644	2	Q4PQS7_9HEPC	Q4pq8 hepatitis c
946	80.5	4.6	1804	1	COBA1_MOUSE	Q61245 mus musculu
947	80.5	4.6	1804	2	Q80WR4_MOUSE	Q80wr4 mus musculu
948	80.5	4.6	1911	2	Q29528_PAPHA	Q29528 papio hamad
949	80.5	4.6	1928	2	Q4PE06_USTMA	Q4pe06 ustilago ma
950	80.5	4.6	2039	1	CR1_HUMAN	P17927 homo sapien
951	80.5	4.6	2039	2	Q5SR43_HUMAN	Q5sr43 homo sapien
952	80.5	4.6	2039	2	Q5SR44_HUMAN	Q5sr44 homo sapien
953	80.5	4.6	2039	2	Q5SR45_HUMAN	Q5sr45 homo sapien
954	80.5	4.6	2322	2	Q6UDW6_PLAFA	Q6udw6 plasmodium
955	80.5	4.6	4199	2	P74440_SYNY3	P74440 synechocyst
956	80	4.6	166	2	Q7PAW6_RICSI	Q7paw6 rickettsia
957	80	4.6	177	2	Q6EKX1_BIOGL	Q6ekx1 biophalari
958	80	4.6	177	2	Q6EKX5_BIOGL	Q6ekx5 biophalari
959	80	4.6	217	2	Q95UV7_BIOGL	Q95uv7 biophalari
960	80	4.6	297	2	O34879_BACSU	O34879 bacillus su
961	80	4.6	308	2	Q5FWS0_XENTR	Q5fws0 xenopus tro
962	80	4.6	310	2	Q5U6G7_BETVU	Q5u6g7 beta vulgar
963	80	4.6	318	2	Q6ZNF8_HUMAN	Q6znf8 homo sapien
964	80	4.6	318	2	Q6ZQW8_HUMAN	Q6zqw8 homo sapien
965	80	4.6	355	2	Q5CQX2_CRYPV	Q5cq2 cryptospori
966	80	4.6	395	1	DNAJ2_CORGL	Q8nly8 crynebacte
967	80	4.6	397	2	Q5AXX1_EMENI	Q5axx1 aspergillus
968	80	4.6	398	2	Q4UGB1_THEAN	Q4ugb1 theileria a
969	80	4.6	405	1	PDC2_PEA	P51851 pium sativ
970	80	4.6	411	2	Q54TD6_DICDI	Q54td6 dictyosteli
971	80	4.6	414	2	Q5V6U3_HALMA	Q5v6u3 haloarcula
972	80	4.6	426	2	Q6ZS27_HUMAN	Q6z827 homo sapien
973	80	4.6	426	2	Q5XNJ5_9HEPC	Q5xnj5 hepatitis c
974	80	4.6	426	2	Q5XNK3_9HEPC	Q5xnk3 hepatitis c
975	80	4.6	439	1	FGL2_HUMAN	Q14314 homo sapien
976	80	4.6	439	2	Q53GD2_HUMAN	Q53gd2 homo sapien
977	80	4.6	439	2	Q5P3I1_CHICK	Q5f3i1 gallus gall
978	80	4.6	454	2	Q8GXT3_ARATH	Q8gxt3 arabidopsis
979	80	4.6	489	2	Q743I3_MYCPA	Q743i3 mycobacteri
980	80	4.6	497	2	Q4NL96_9MICC	Q4nl96 arthrobacte

Q9rl82	mus musculus
O70605	rattus norv
P06874	bacillus st
Q4kp36	hepatitis c
Q4kp37	hepatitis c
Q4kp38	hepatitis c
Q4kp39	hepatitis c
Q4kp45	hepatitis c
Q4hu61	gibberella
Q7qbp4	anopheles g
Q8edm8	shewanella
Q4hxl9	gibberella
Q04184	hepatitis c
Q934j0	paenibacill
Q80b16	hepatitis c
Q9zj88	helicobacte
P77468	escherichia
Q7agt8	escherichia
Q8xct4	escherichia
Q6xli6	fugu rubrip
Q6cfi8	yarrowia li
Q21750	caenorhabdi
P54763	mus musculus
Q9hlq9	thermoplasm
Q58m71	cyanophage
Q6gtq7	mus musculus
Q6p5f1	mus musculus
Q8a2y1	bacteroides
Q8v291	venezuelan
Q88979	venezuelan
Q8v293	venezuelan
Q9ykd3	venezuelan
Q5ibc2	venezuelan
Q8uyh1	venezuelan
Q5b7i5	aspergillus
Q4pqu7	hepatitis c
Q4pq88	hepatitis c
Q4pq87	hepatitis c
Q61245	mus musculus
Q80wr4	mus musculus
Q29528	papio hamad
Q4pe06	ustilago ma
P17927	homo sapien
Q5sr43	homo sapien
Q5sr44	homo sapien
Q5sr45	homo sapien
Q6udw6	plasmodium
P74440	synechocyst
Q7paw6	rickettsia
Q6kx11	biomphalari
Q6ekx5	biomphalari
Q95uv7	biomphalari
Q34879	biomphalari
Q34879	biomphalari
Q5fws0	xenopus tro
Q5u6g7	beta vulgar
Q6znf8	homo sapien
Q6zqw8	homo sapien
Q5cqx2	cryptospori
Q8nly8	corynebacte
Q5axx1	aspergillus
Q4ugb1	theileria a
P51851	pisum sativ
Q54td6	dictyosteli
Q5v6u3	haloarcula
Q6z827	homo sapien
Q5xnj5	hepatitis c
Q5xnk3	hepatitis c
Q14314	homo sapien
Q53gd2	homo sapien
Q5f3i1	gallus gall
Q8gxt3	arabidopsis
Q743i3	mycobacteri
Q4nl96	arthrobacte

981	80	4.6	519	2	Q55JJ6_CRYNE	Q55jj6 cryptococcus	1054	79.5	4.6	426	2	Q5XNV3_9HEPC	Q5xmv3 hepatitis c
982	80	4.6	519	2	Q5KA05_CRYNE	Q5ka05 cryptococcus	1055	79.5	4.6	426	2	Q5XNW4_9HEPC	Q5xmw4 hepatitis c
983	80	4.6	534	2	Q9REJ1_ACEDI	Q9rbj1 acetobacter	1056	79.5	4.6	426	2	Q5XNW7_9HEPC	Q5xmw7 hepatitis c
984	80	4.6	538	2	Q74D86_GEOSL	Q74d86 geobacter s	1057	79.5	4.6	426	2	Q5XMX0_9HEPC	Q5xmx0 hepatitis c
985	80	4.6	561	2	Q82764_9INFA	Q82764 influenza a	1058	79.5	4.6	426	2	Q5XMX2_9HEPC	Q5xmx2 hepatitis c
986	80	4.6	565	2	Q82766_9INFA	Q82766 influenza a	1059	79.5	4.6	426	2	Q5XN32_9HEPC	Q5xn32 hepatitis c
987	80	4.6	566	2	Q8UWT0_9INFA	Q8uwt0 influenza a	1060	79.5	4.6	426	2	Q5XN55_9HEPC	Q5xn55 hepatitis c
988	80	4.6	574	2	Q8E9W9_SHEON	Q8e9w9 shewanella	1061	79.5	4.6	426	2	Q5XN57_9HEPC	Q5xn57 hepatitis c
989	80	4.6	576	2	Q5B821_SHEONI	Q5b821 aspergillus	1062	79.5	4.6	426	2	Q5XN62_9HEPC	Q5xn62 hepatitis c
990	80	4.6	576	2	Q7W637_BORPA	Q7w637 bordetella	1063	79.5	4.6	426	2	Q5XN92_9HEPC	Q5xn92 hepatitis c
991	80	4.6	576	2	Q7WI03_BORBR	Q7wi03 bordetella	1064	79.5	4.6	426	2	Q5XN93_9HEPC	Q5xn93 hepatitis c
992	80	4.6	577	2	Q9L5C5_BURPS	Q9l5c5 burkholderi	1065	79.5	4.6	426	2	Q5XNB4_9HEPC	Q5xnb4 hepatitis c
993	80	4.6	580	2	Q4QRJ7_BRARE	Q4qrj7 brachydanio	1066	79.5	4.6	441	1	TOLB_ANAMM	Q5xnb4 hepatitis c
994	80	4.6	582	2	Q4V3B3_ARATH	Q4v3b3 arabidopsis	1067	79.5	4.6	474	2	Q8L0Y4_9MICO	Q5pbh8 anaplasma m
995	80	4.6	584	2	Q4V706_DROME	Q4v706 drosophila	1068	79.5	4.6	482	2	Q6NVW1_HUMAN	Q8l0y4 terrabacter
996	80	4.6	593	2	Q8RUU6_MAIZE	Q8ruu6 zea mays (m	1069	79.5	4.6	500	2	Q759N6_ASHGO	Q6nvw1 homo sapien
997	80	4.6	597	2	Q9LGL5_ORYSA	Q9lgl5 oryza sativ	1070	79.5	4.6	507	2	Q88983_9RHAB	Q759n6 ashbya goss
998	80	4.6	641	1	FIBA2_PETMA	P33573 petromyzon	1071	79.5	4.6	517	2	Q93ZQ4_ARATH	Q88983 viral hemor
999	80	4.6	670	2	Q9FCR7_NEIMB	Q9fcr7 neisseria m	1072	79.5	4.6	536	2	Q93ZQ4_ARATH	Q93zq4 arabidopsis
1000	80	4.6	671	2	Q8SXR9_DROME	Q8sxr9 drosophila	1073	79.5	4.6	566	2	Q4PC63_USTMA	Q4pc63 ustilago ma
1001	80	4.6	702	2	Q9TMV8_9POAL	Q9tmv8 guaduelia m	1074	79.5	4.6	586	2	Q9YTB9_9INFA	Q9ytb9 influenza a
1002	80	4.6	702	2	Q69749_NEIME	Q69749 neisseria m	1075	79.5	4.6	606	2	Q84XV1_MUSAC	Q84xv1 musa acumin
1003	80	4.6	737	2	Q7M9D6_WOLSU	Q7m9d6 wolinnella s	1076	79.5	4.6	626	2	Q64599_ARATH	Q8xp99 clostridium
1004	80	4.6	762	2	Q4I8H9_GIBZE	Q4i8h9 gibberella	1077	79.5	4.6	672	2	Q613K3_CAEBR	O64599 arabidopsis
1005	80	4.6	765	2	Q50YB3_ENTHI	Q50yb3 entamoeba h	1078	79.5	4.6	691	2	Q4SVM2_TETNG	Q613k3 caenorhabdi
1006	80	4.6	766	2	Q82K66_STRAW	Q82k66 streptomyce	1079	79.5	4.6	706	1	TGM3L_HUMAN	Q4svm2 tetraodon n
1007	80	4.6	767	2	Q5WIY5_BACSK	Q5wiy5 bacillus cl	1080	79.5	4.6	712	2	Q6FDG4_ACIAD	O95932 homo sapien
1008	80	4.6	771	2	Q8NXX6_9FUNG	Q8njx6 piromyces s	1081	79.5	4.6	726	2	Q59HH9_VIBVU	Q6fdg4 acinetobact
1009	80	4.6	778	2	Q8NXX5_9FUNG	Q8njx5 piromyces s	1082	79.5	4.6	746	2	Q8JPM2_9HEPC	Q59hh9 vibrio vuln
1010	80	4.6	811	2	Q5REB3_PONPY	Q5rbn3 pongo pygma	1083	79.5	4.6	750	2	Q41103_PHAVU	Q8jpm2 hepatitis c
1011	80	4.6	815	2	Q41553_WHEAT	Q41553 triticum ae	1084	79.5	4.6	791	2	Q7XA15_WHEAT	Q41103 phaseolus v
1012	80	4.6	862	2	Q7N9C5_PHOLL	Q7n9c5 photorhabdu	1085	79.5	4.6	791	2	Q7XA15_WHEAT	Q7xa15 triticum ae
1013	80	4.6	902	1	FTHFD_PONPY	Q5rfm9 pongo pygma	1086	79.5	4.6	796	2	Q7XA16_AEGTA	Q7xa16 aegilops ta
1014	80	4.6	946	2	Q96163_PLAF7	Q96163 plasmodium	1087	79.5	4.6	867	2	Q9A3S5_CAUCR	Q9a3s5 caulobacter
1015	80	4.6	955	2	Q8A654_BACTN	Q8a654 bacteroides	1088	79.5	4.6	922	2	Q6PAE2_XENLA	Q6pae2 xenopus lae
1016	80	4.6	1016	2	Q91779_XENLA	Q91779 xenopus lae	1089	79.5	4.6	946	2	Q5GYV2_XANOR	Q5gyv2 xanthomonas
1017	80	4.6	1258	2	Q8AW11_BRARE	Q8awl1 brachydanio	1090	79.5	4.6	972	2	Q5TFU3_HUMAN	Q5tfu3 homo sapien
1018	80	4.6	1306	2	Q93N36_PANAN	Q93n36 pantoea ana	1091	79.5	4.6	986	2	Q5T0U6_HUMAN	Q5t0u6 homo sapien
1019	80	4.6	1519	2	Q48237_HELUMU	Q48237 helicobacte	1092	79.5	4.6	987	2	Q5T0U8_HUMAN	Q5t0u8 homo sapien
1020	80	4.6	1519	2	Q4PQQ6_9HEPC	Q4pqg6 hepatitis c	1093	79.5	4.6	988	2	O64454_ORYSA	P93416 oryza sativ
1021	80	4.6	1641	2	Q5LJZ2_DROME	Q5ljz2 drosophila	1094	79.5	4.6	1004	2	Q4LE53_HUMAN	Q5t0u8 homo sapien
1022	80	4.6	1646	2	Q4PQU2_9HEPC	Q4pqu2 hepatitis c	1095	79.5	4.6	1055	1	EPHB2_HUMAN	O64454 oryza sativ
1023	80	4.6	1694	2	Q8SA88_MAIZE	Q8sa88 zea mays (m	1096	79.5	4.6	1055	2	Q5T0U7_HUMAN	Q4le53 homo sapien
1024	80	4.6	1746	1	TENA_PIG	Q29116 sus scrofa	1097	79.5	4.6	1136	2	Q8K2V0_MOUSE	P29323 homo sapien
1025	80	4.6	1844	2	Q4FYM5_LEIMA	Q4fym5 leishmania	1098	79.5	4.6	1136	2	Q8C109_MOUSE	Q5t0u7 homo sapien
1026	80	4.6	1880	2	Q9DKW2_9CALI	Q9dkw2 walrus cali	1099	79.5	4.6	1136	2	Q5XXE0_MOUSE	Q8k2v0 mus musculu
1027	80	4.6	3010	2	P90195_9HEPC	P90195 hepatitis c	1100	79.5	4.6	1175	2	Q9SWE0_MAIZE	Q8c109 mus musculu
1028	80	4.6	3010	2	Q9U3I1_9HEPC	Q9j3i1 hepatitis c	1101	79.5	4.6	1196	1	AMVB_PAEPO	Q5xke0 mus musculu
1029	80	4.6	3586	2	Q70KJ6_BACAM	Q70kj6 bacillus am	1102	79.5	4.6	1224	2	Q7T0Z4_BRARE	Q9swe0 zea mays (m
1030	80	4.6	3843	2	Q9U5D0_DROME	Q9u5d0 drosophila	1103	79.5	4.6	1323	2	Q8Y1G6_RALSO	P21543 paenibacill
1031	80	4.6	3843	2	Q9VU94_DROME	Q9vu94 drosophila	1104	79.5	4.6	1324	2	Q64T13_BACFR	Q7t024 brachydanio
1032	79.5	4.6	200	2	Q70603_RAT	Q70603 rattus norv	1105	79.5	4.6	1389	2	Q4SGS3_TETNG	Q8y1g6 ralstonia s
1033	79.5	4.6	237	2	Q31175_NEIME	Q31175 neisseria m	1106	79.5	4.6	1644	2	Q4PQT1_9HEPC	Q64ti3 bacteroides
1034	79.5	4.6	241	2	Q9AE80_NEIME	Q9ae80 neisseria m	1107	79.5	4.6	1955	2	Q7S0A7_NEUCR	Q4sgs3 tetraodon n
1035	79.5	4.6	241	2	O07273_NEIME	O07273 neisseria m	1108	79.5	4.6	2236	1	PYR1_DROME	Q4pgt1 hepatitis c
1036	79.5	4.6	241	2	O07274_NEIME	O07274 neisseria m	1109	79.5	4.6	2489	2	Q16744_HUMAN	Q7s0a7 neurospora
1037	79.5	4.6	241	2	O07912_NEIME	O07912 neisseria m	1110	79.5	4.6	2761	2	Q18447_CAEEL	P05990 drosophila
1038	79.5	4.6	254	2	Q9MS16_9POAL	Q9msl6 diptatherum	1111	79.5	4.6	3011	2	Q9ELS8_9HEPC	Q16744 homo sapien
1039	79.5	4.6	255	2	Q8PHU4_XANAC	Q8phu4 xanthomonas	1112	79.5	4.6	3013	2	Q9QIX9_9HEPC	Q18447 caenorhabdi
1040	79.5	4.6	270	2	Q9RQV4_NEIME	Q9rqv4 neisseria m	1113	79.5	4.6	3412	2	Q87PW3_VIBPA	Q9el88 hepatitis c
1041	79.5	4.6	284	2	Q5TPH3_ANOGA	Q5tph3 anopheles g	1114	79.5	4.6	3531	2	Q7N1Z0_PHOLL	Q9qix9 hepatitis c
1042	79.5	4.6	301	2	Q7SZ01_XENLA	Q7sz01 xenopus lae	1115	79	4.5	323	2	Q7NMB1_GLOVI	Q87pw3 vibrio para
1043	79.5	4.6	323	2	Q29041_PIG	Q29041 sus scrofa	1116	79	4.5	338	2	Q5HXM2_GLUOX	Q7n1z0 photorhabdu
1044	79.5	4.6	326	2	Q9WG51_9HEPC	Q9wg51 hepatitis c	1117	79	4.5	343	2	Q7ZXL3_XENLA	Q7nmb1 gluobacter
1045	79.5	4.6	329	2	Q6DIX5_XENTR	Q6dix5 xenopus tro	1118	79	4.5	371	2	Q8UUS7_9GOBI	Q5hxm2 gluconobact
1046	79.5	4.6	335	1	FCN1_RAT	Q9wt88 rattus norv	1119	79	4.5	372	2	Q800W4_CHICK	Q7zx13 xenopus lae
1047	79.5	4.6	335	2	Q5M8B4_RAT	Q5m8b4 rattus norv	1120	79	4.5	375	2	Q63YZ9_BURPS	Q8uus7 bostrychus
1048	79.5	4.6	372	1	AGI_URTDI	P11218 urtica dioi	1121	79	4.5	375	2	Q62GH0_BURMA	Q800w4 gallus gall
1049	79.5	4.6	372	2	Q9SYR1_URTDI	Q9syrl urtica dioi	1122	79	4.5	405	2	Q4S6P4_TETNG	Q63yz9 burkholderi
1050	79.5	4.6	388	2	Q9U307_CAEEL	Q9u307 caenorhabdi	1123	79	4.5	414	1	NAS26_CAEEL	Q62gh0 burkholderi
1051	79.5	4.6	399	2	Q4P8N6_USTMA	Q4p8n6 ustilago ma	1124	79	4.5	431	2	Q86H05_BIOGL	Q4s6p4 tetraodon n
1052	79.5	4.6	426	2	Q5XMM5_9HEPC	Q5xmm5 hepatitis c	1125	79	4.5	448	2	Q8DMZ4_STRR6	Q22710 caenorhabdi
1053	79.5	4.6	426	2	Q5XMT2_9HEPC	Q5xmt2 hepatitis c	1126	79	4.5	456	2	Q6AA53_PROAC	Q86h05 biophtococc
													Q6aa53 propionibac



1127	79	4.5	466	2	Q81QK6_BACAN	Q81qk6	1200	78.5	4.5	426	2	Q5XNH6_9HEPC	Q5xnh6
1128	79	4.5	490	2	Q4W8M3_9BACI	Q4w8m3	1201	78.5	4.5	440	2	Q8W546_WHEAT	Q8w546
1129	79	4.5	507	1	ALDH_STRCO	Q9rjz6	1202	78.5	4.5	453	2	Q526H2_MAGGR	Q526h2
1130	79	4.5	513	2	Q5CXR6_CRYPV	Q5cxr6	1203	78.5	4.5	466	2	Q82M96_STRAW	Q82m96
1131	79	4.5	519	2	Q9RQT8_9SPHI	Q9rqt8	1204	78.5	4.5	473	2	Q5M8I5_XENTR	Q5m8i5
1132	79	4.5	531	2	Q97T17_CLOAB	Q97ti7	1205	78.5	4.5	479	2	Q8GN31_ERWCH	Q8gn31
1133	79	4.5	535	2	Q8PXS1_METWA	Q8pxs1	1206	78.5	4.5	482	1	COBA1_RAT	Q20909
1134	79	4.5	544	2	P74655_SYNY3	P74655	1207	78.5	4.5	491	2	Q6CMT5_KLULA	Q6cmt5
1135	79	4.5	551	2	Q4QNR4_HAEI8	Q4qnr4	1208	78.5	4.5	491	2	Q9F0I2_PSECL	Q9f0i2
1136	79	4.5	555	2	Q6IEQ7_ORYSA	Q6ieq7	1209	78.5	4.5	494	2	Q7T839_9VIRU	Q7t839
1137	79	4.5	565	2	Q8JUUS_9INFA	Q8juu5	1210	78.5	4.5	509	2	Q8WS99_9ECHI	Q8ws99
1138	79	4.5	566	2	Q8UWT1_9INFA	Q8uwt1	1211	78.5	4.5	531	2	Q8G7R4_BIFLO	Q8g7r4
1139	79	4.5	605	2	Q8S4W8_MAIZE	Q8s4w8	1212	78.5	4.5	551	2	Q8WP18_MACFA	Q8wp18
1140	79	4.5	605	2	Q9FVF0_FRAAN	Q9fvf0	1213	78.5	4.5	566	2	Q82752_9ORTO	Q82752
1141	79	4.5	606	2	Q8S4W9_MAIZE	Q8s4w9	1214	78.5	4.5	566	2	Q82774_9INFA	Q82774
1142	79	4.5	625	1	TNR11_MOUSE	Q35305	1215	78.5	4.5	568	2	Q5BJV4_RAT	Q5bjv4
1143	79	4.5	642	2	Q5BGY6_EMENI	Q5bgy6	1216	78.5	4.5	576	2	Q4KP42_9HEPC	Q4kp42
1144	79	4.5	646	2	Q6ZN80_HUMAN	Q6zn80	1217	78.5	4.5	622	2	Q6D8P1_ERWCT	Q6d8p1
1145	79	4.5	649	2	Q8YD80_BRUME	Q8yd80	1218	78.5	4.5	626	2	P92990_ARATH	P92990
1146	79	4.5	676	2	Q579L1_BRUAB	Q579l1	1219	78.5	4.5	655	2	Q8WQX8_BIOGL	Q8wx8
1147	79	4.5	676	2	Q8FV51_BRUSU	Q8fv51	1220	78.5	4.5	661	2	Q8A103_BACTN	Q8a103
1148	79	4.5	689	2	Q5LDX1_BACFN	Q5ldx1	1221	78.5	4.5	673	2	Q4RKJ4_TETNG	Q4rkj4
1149	79	4.5	689	2	Q64V15_BACFR	Q64v15	1222	78.5	4.5	698	1	YMCA_ECOLI	P75882
1150	79	4.5	701	2	Q9T2A4_9POAL	Q9t2a4	1223	78.5	4.5	698	2	O48900_MAIZE	O48900
1151	79	4.5	702	2	Q9T2A1_OTAAC	Q9t2a1	1224	78.5	4.5	764	2	O8VWN0_WHEAT	O8vwn0
1152	79	4.5	730	2	Q4XEX1_PLACH	Q4xex1	1225	78.5	4.5	764	2	O68881_PSEAB	O68881
1153	79	4.5	747	2	Q98L70_RHILO	Q98l70	1226	78.5	4.5	764	2	O9HV88_PSEAB	O9hv88
1154	79	4.5	759	2	Q51NS3_MAGGR	Q51ns3	1227	78.5	4.5	770	1	GLGB_STNY3	P52981
1155	79	4.5	776	2	Q18696_CAEEL	Q18696	1228	78.5	4.5	781	2	Q9XAL9_STRCO	Q9xal9
1156	79	4.5	835	2	Q99PX3_ECOLI	Q99px3	1229	78.5	4.5	790	2	Q8W547_WHEAT	Q8w547
1157	79	4.5	874	2	Q4UFV5_THEAN	Q4ufv5	1230	78.5	4.5	804	2	Q6ZQE3_MOUSE	Q6zqe3
1158	79	4.5	902	2	Q53HP5_HUMAN	Q53hp5	1231	78.5	4.5	823	2	Q6LR67_PHOPR	Q6lr67
1159	79	4.5	919	1	HEX_ADE12	P19900	1232	78.5	4.5	837	2	Q9A3Q6_CAUCR	Q9a3q6
1160	79	4.5	971	2	Q9ZE42_RICPR	Q9ze42	1233	78.5	4.5	853	2	Q6IPK3_HUMAN	Q6ipk3
1161	79	4.5	1374	2	Q6FPQ7_CANGA	Q6fpq7	1234	78.5	4.5	870	2	Q6FC24_ACIAD	Q6fc24
1162	79	4.5	1472	2	Q87B49_XYLFT	Q87b49	1235	78.5	4.5	883	2	Q4XEH8_PLACH	Q4xeh8
1163	79	4.5	1480	2	Q4TU93_RAT	Q4tu93	1236	78.5	4.5	900	1	MANBA_CAEEL	Q93324
1164	79	4.5	1644	2	Q4POS5_9HEPC	Q4pq85	1237	78.5	4.5	914	2	O29964_ARCFU	O29964
1165	79	4.5	1644	2	Q4PQP7_9HEPC	Q4ppq7	1238	78.5	4.5	922	2	Q8PLC0_XANAC	Q8plc0
1166	79	4.5	2326	2	Q6BRQ7_DBEHA	Q6brq7	1239	78.5	4.5	989	2	Q9PWN6_CHICK	Q9pwn6
1167	78.5	4.5	300	1	MRW_CHLTR	O84274	1240	78.5	4.5	990	2	Q8LNN7_ORYSA	Q8lnn7
1168	78.5	4.5	302	1	MRW_CHLMU	Q9pkc2	1241	78.5	4.5	993	2	Q9L036_STRCO	Q9l036
1169	78.5	4.5	307	2	Q28703_RABIT	Q28703	1242	78.5	4.5	1005	1	TARP1_CHLTR	O84462
1170	78.5	4.5	308	2	Q7QHK9_ANOGA	Q7qhk9	1243	78.5	4.5	1014	2	Q8WPI7_MACFA	Q8wpi7
1171	78.5	4.5	312	2	Q625S0_CAEER	Q625s0	1244	78.5	4.5	1015	2	Q4UWG2_XANCP	Q4uwg2
1172	78.5	4.5	312	2	Q5RSB2_PONPY	Q5rsb2	1245	78.5	4.5	1015	2	Q8P7N8_XANCP	Q8p7n8
1173	78.5	4.5	326	2	Q98UT5_9HEPC	Q98ut5	1246	78.5	4.5	1020	2	Q7Q204_ANOGA	Q7q204
1174	78.5	4.5	326	2	Q98V73_9HEPC	Q98v73	1247	78.5	4.5	1137	1	BCSC_ECO57	Q8x5m0
1175	78.5	4.5	354	2	Q5ZK00_CHICK	Q5zk00	1248	78.5	4.5	1139	1	HMW1_MYCGE	Q49413
1176	78.5	4.5	360	2	Q68DD1_HUMAN	Q68dd1	1249	78.5	4.5	1191	2	O4S4D3_TETNG	Q4s4d3
1177	78.5	4.5	368	2	Q4IXP0_AZOVI	Q4ixp0	1250	78.5	4.5	1234	2	O77285_DROME	O77285
1178	78.5	4.5	372	2	Q7ZVF2_BRARE	Q7zvf2	1251	78.5	4.5	1234	2	Q9W0B8_DROME	Q9w0b8
1179	78.5	4.5	380	2	Q9FUR8_LYCES	Q9fur8	1252	78.5	4.5	1248	1	TPP2_RAT	Q64560
1180	78.5	4.5	387	2	O18546_BIOGL	O18546	1253	78.5	4.5	1249	2	Q5D072_MOUSE	Q5d072
1181	78.5	4.5	394	2	Q9W6E6_9TELE	Q9w6e6	1254	78.5	4.5	1261	1	TPP2_MOUSE	Q64514
1182	78.5	4.5	403	2	Q6DDX1_XENLA	Q6ddk1	1255	78.5	4.5	1363	2	Q8BZ47_MOUSE	Q8bz47
1183	78.5	4.5	409	2	Q9SP05_LYCES	Q9sp05	1256	78.5	4.5	1395	2	Q9AIS0_9STAP	Q9ais0
1184	78.5	4.5	412	2	Q9ZQR5_ARATH	Q9zqr5	1257	78.5	4.5	1436	1	WC11_BOVIN	P30205
1185	78.5	4.5	414	2	Q749U8_GEOSL	Q749u8	1258	78.5	4.5	1506	2	Q54U77_DICTDI	Q54u77
1186	78.5	4.5	423	2	Q7Z1Z8_DICTDI	Q7z1z8	1259	78.5	4.5	1549	2	Q6MIW7_DDEBA	Q6miw7
1187	78.5	4.5	426	2	Q5XMM4_9HEPC	Q5xmm4	1260	78.5	4.5	1595	2	Q6MNM4_BDEBA	Q6mnk4
1188	78.5	4.5	426	2	Q5XMM6_9HEPC	Q5xmm6	1261	78.5	4.5	1766	2	Q8AW45_BRARE	Q8aw45
1189	78.5	4.5	426	2	Q5XMT0_9HEPC	Q5xmt0	1262	78.5	4.5	1838	2	Q15094_HUMAN	Q15094
1190	78.5	4.5	426	2	Q5XMU2_9HEPC	Q5xmu2	1263	78.5	4.5	2014	2	Q29530_PANTR	Q29530
1191	78.5	4.5	426	2	Q5XN46_9HEPC	Q5xn46	1264	78.5	4.5	2221	2	Q73BZ3_BACC1	Q73bz3
1192	78.5	4.5	426	2	Q5XN47_9HEPC	Q5xn47	1265	78.5	4.5	2481	1	FINC_XENLA	Q91740
1193	78.5	4.5	426	2	Q5XN85_9HEPC	Q5xn85	1266	78.5	4.5	2481	2	Q6GQA5_XENLA	Q6gqa5
1194	78.5	4.5	426	2	Q5XNA0_9HEPC	Q5xna0	1267	78.5	4.5	2653	2	Q25253_LUCCTU	Q25253
1195	78.5	4.5	426	2	Q5XNA1_9HEPC	Q5xna1	1268	78.5	4.5	4417	2	Q582D2_9TRYP	Q582d2
1196	78.5	4.5	426	2	Q5XNA2_9HEPC	Q5xna2	1269	78	4.5	176	2	Q6EKX3_BIOGL	Q6ekx3
1197	78.5	4.5	426	2	Q5XNCL_9HEPC	Q5xnc1	1270	78	4.5	267	2	Q8K583_RAT	Q8k583
1198	78.5	4.5	426	2	Q5XND1_9HEPC	Q5xnd1	1271	78	4.5	310	2	Q6CYZ3_ERWCT	Q6cyz3
1199	78.5	4.5	426	2	Q5XNH3_9HEPC	Q5xnh3	1272	78	4.5	317	2	Q93WY7_TOBAC	Q93wy7

1273	78	4.5	318	2	Q95YH3_9EUKA	Q95yh3 pseudotrich	1346	77.5	4.4	257	2	Q5YB91_9SPHN	Q5yb91 sphingomona
1274	78	4.5	321	2	Q6NJ01_CORDI	Q6nj01 corynebacte	1347	77.5	4.4	271	2	Q7UXU2_RHOBA	Q7uxu2 rhodopirell
1275	78	4.5	344	2	Q8MNB1_DICDI	Q8mnb1 dictyosteli	1348	77.5	4.4	306	2	Q5FVU9_XENTR	Q5fvu9 xenopus tro
1276	78	4.5	349	2	Q04676_HORVU	Q04676 hordeum vul	1349	77.5	4.4	315	2	Q7MUB0_PORGI	Q7mub0 porphyromon
1277	78	4.5	351	2	Q93PW0_PARPN	Q93pw0 paracoccusc	1350	77.5	4.4	324	2	Q9FEW1_NICSY	Q9few1 nicotiana s
1278	78	4.5	360	2	Q67QI2_SYMTH	Q67qi2 symbiobacte	1351	77.5	4.4	326	2	Q9WG50_9HEPC	Q9wg50 hepatitis c
1279	78	4.5	371	2	Q8UUS6_9GOBI	Q8uus6 bostrychus	1352	77.5	4.4	326	2	Q9WG54_9HEPC	Q9wg54 hepatitis c
1280	78	4.5	387	2	Q6E202_RIEAN	Q6e202 riemerella	1353	77.5	4.4	334	2	Q6OLK8_CAEBR	Q6olk8 caenorhabdi
1281	78	4.5	396	2	Q88GZ5_PSEPK	Q88gz5 pseudomonas	1354	77.5	4.4	405	1	ANGL4_RAT	Q6tma8 rattus norv
1282	78	4.5	397	2	Q9FZ50_ARATH	Q9fz50 arabidopsis	1355	77.5	4.4	410	1	ANGL4_MOUSE	Q9z1p8 mus musculu
1283	78	4.5	404	2	Q22791_ARATH	Q22791 arabidopsis	1356	77.5	4.4	410	2	Q78ZJ9_MOUSE	Q78zj9 mus musculu
1284	78	4.5	423	2	Q8GY81_ARATH	Q8gy81 arabidopsis	1357	77.5	4.4	423	2	Q55FW5_DICDI	Q55fw5 dictyosteli
1285	78	4.5	453	2	Q6MR90_BDEBA	Q6mr90 bdellovibri	1358	77.5	4.4	426	2	Q5XNV0_9HEPC	Q5xmv0 hepatitis c
1286	78	4.5	497	2	Q6BMV1_DEBHA	Q6bmvl debaryomyce	1359	77.5	4.4	426	2	Q5XNV9_9HEPC	Q5xmv9 hepatitis c
1287	78	4.5	507	2	Q6QDI5_9RHAB	Q6qdi5 viral hemor	1360	77.5	4.4	426	2	Q5XNM6_9HEPC	Q5xmw6 hepatitis c
1288	78	4.5	511	2	Q60637_MOUSE	Q60637 mus musculu	1361	77.5	4.4	426	2	Q5XN27_9HEPC	Q5xn27 hepatitis c
1289	78	4.5	544	2	Q9NUL8_HUMAN	Q9nul8 homo sapien	1362	77.5	4.4	426	2	Q5XN94_9HEPC	Q5xn94 hepatitis c
1290	78	4.5	559	2	Q6DX25_9INFPA	Q6dx25 influenza a	1363	77.5	4.4	426	2	Q5XNH9_9HEPC	Q5xnh9 hepatitis c
1291	78	4.5	571	2	Q9EY44_CELUD	Q9ey44 cellulomona	1364	77.5	4.4	455	2	Q8VZ33_ARATH	Q8vz33 arabidopsis
1292	78	4.5	581	2	Q640P8_MOUSE	Q640p8 mus musculu	1365	77.5	4.4	456	2	Q7UXP2_RHOBA	Q7uxp2 rhodopirell
1293	78	4.5	584	2	Q81118_WHEAT	Q81118 triticum ae	1366	77.5	4.4	464	2	Q9FWK8_ORYSA	Q9fwk8 oryza sativ
1294	78	4.5	586	2	Q8BJW6_MOUSE	Q8bjw6 m mus muscu	1367	77.5	4.4	464	2	Q7XDI5_ORYSA	Q7xd15 oryza sativ
1295	78	4.5	623	2	Q7SZG1_FUGRU	Q7szg1 fugu rubrip	1368	77.5	4.4	472	2	Q673V5_9GAMM	Q673v5 solemya vel
1296	78	4.5	625	2	Q7Z867_USTMA	Q7z867 ustilago ma	1369	77.5	4.4	491	1	ANGL1_HUMAN	Q95841 homo sapien
1297	78	4.5	625	2	Q4PG50_USTMA	Q4pg50 ustilago ma	1370	77.5	4.4	491	2	Q53F22_HUMAN	Q53f22 homo sapien
1298	78	4.5	641	2	Q4LV49_9BURK	Q4lv49 burkholderi	1371	77.5	4.4	559	2	Q84BN2_9CELL	Q84bn2 cellulomona
1299	78	4.5	647	2	Q8A1K0_BACTN	Q8alk0 bacteroides	1372	77.5	4.4	570	2	Q6U9J2_9CAUD	Q6u9j2 bacterioph
1300	78	4.5	666	1	NEPUL1_THEVU	Q60053 thermoactin	1373	77.5	4.4	577	2	Q64880_ARATH	Q64880 arabidopsis
1301	78	4.5	675	2	Q4I2V4_GIBZE	Q4i2v4 gibberella	1374	77.5	4.4	580	2	Q4X079_ASPFU	Q4x079 aspergillus
1302	78	4.5	675	2	Q32045_9POAL	Q32045 cephalostac	1375	77.5	4.4	586	2	Q94019_CANAL	Q94019 candida alb
1303	78	4.5	706	2	Q898P2_CLOTE	Q898p2 clostridium	1376	77.5	4.4	597	1	DFA3_SYNY3	P74373 synechocyst
1304	78	4.5	730	2	Q5H0V1_XANOR	Q5h0v1 xanthomonas	1377	77.5	4.4	606	2	Q84V95_LOTCO	Q84v95 lotus corni
1305	78	4.5	743	2	E13B_TRIHA	P53626 trichoderma	1378	77.5	4.4	627	2	Q6ZA27_ORYSA	Q6za27 oryza sativ
1306	78	4.5	762	1	Q8SD31_9CAUD	Q8sd31 pseudomonas	1379	77.5	4.4	635	1	SYT_XYLFA	Q9pfe2 xylella fas
1307	78	4.5	771	2	Q5DIW0_PSEAE	Q5diw0 pseudomonas	1380	77.5	4.4	635	1	SYT_XYLFT	Q87ab2 xylella fas
1308	78	4.5	785	2	Q4LU26_9BURK	Q4lu26 burkholderi	1381	77.5	4.4	638	2	Q75M14_ORYSA	Q75m14 oryza sativ
1309	78	4.5	786	2	Q9NVE9_HUMAN	Q9nve9 homo sapien	1382	77.5	4.4	640	1	DHSA_YEAST	Q00711 saccharomyc
1310	78	4.5	795	2	Q9UF53_HUMAN	Q9uf53 homo sapien	1383	77.5	4.4	642	2	Q84HJ5_STRMA	Q84hj5 streptomyce
1311	78	4.5	801	1	PI5K1_ORYSA	Q6ex42 oryza sativ	1384	77.5	4.4	677	2	Q9RHR1_KLEPN	Q9xhr1 klebsiella
1312	78	4.5	811	2	Q5KAV3_CRYNE	Q5kav3 cryptococcu	1385	77.5	4.4	682	2	Q4GZ10_9TRYP	Q4gz10 trypanosoma
1313	78	4.5	811	2	Q55KL8_CRYNE	Q55kl8 cryptococcu	1386	77.5	4.4	711	2	Q851C3_ORYSA	Q851c3 oryza sativ
1314	78	4.5	815	1	FPVA_PSEAE	P48632 pseudomonas	1387	77.5	4.4	750	2	Q5NN26_ZYMMO	Q5nn26 zymomonas m
1315	78	4.5	829	2	Q9ZTB6_HORVU	Q9ztb6 hordeum vul	1388	77.5	4.4	754	2	Q8VW52_ECOLI	Q8vw52 escherichia
1316	78	4.5	843	2	Q55VV3_CRYNE	Q55vv3 cryptococcu	1389	77.5	4.4	792	2	Q7PC51_9ALTE	Q7pc51 saccharoph
1317	78	4.5	843	2	Q5KKD5_CRYNE	Q5kkd5 cryptococcu	1390	77.5	4.4	804	2	Q937J5_ECOLI	Q937j5 escherichia
1318	78	4.5	918	2	Q61DS4_CAEBR	Q6lds4 caenorhabdi	1391	77.5	4.4	816	2	Q5BH82_EMENI	Q5bh82 aspergillus
1319	78	4.5	919	2	Q6BUI9_DEBHA	Q6bui9 debaryomyce	1392	77.5	4.4	830	2	Q03872_WHEAT	Q03872 triticum ae
1320	78	4.5	931	2	Q4Y8U9_PLACH	Q4y8u9 plasmodium	1393	77.5	4.4	842	2	O25950_HELPY	O25950 helicobacte
1321	78	4.5	942	1	AMPE_PIG	Q95334 sus scrofa	1394	77.5	4.4	874	2	Q6TF32_RUMAL	Q6tf32 ruminococcu
1322	78	4.5	962	2	Q4K4X8_PSEF5	Q4k4x8 pseudomonas	1395	77.5	4.4	911	2	Q8LT50_9CAUD	Q8lt50 vibriophag
1323	78	4.5	986	1	GUNZ_CLOSR	P23659 clostridium	1396	77.5	4.4	929	2	Q6AMC7_DESPS	Q6amc7 desulfotale
1324	78	4.5	1015	2	Q4NLL2_9MICC	Q4nll2 archrobacte	1397	77.5	4.4	962	2	Q8GHD8_9ACTO	Q8ghd8 streptomyce
1325	78	4.5	1060	2	Q64YL2_BACFR	Q64yl2 bacteroides	1398	77.5	4.4	993	2	P96992_STRLI	P96992 streptomyce
1326	78	4.5	1083	2	Q51CE3_ENTHI	Q51ce3 entamoeba h	1399	77.5	4.4	995	2	Q8K2R3_MOUSE	Q8k2r3 mus musculu
1327	78	4.5	1206	2	Q869X8_DICDI	Q869x8 dictyosteli	1400	77.5	4.4	1052	2	Q8A3I6_BACTN	Q8a3i6 bacteroides
1328	78	4.5	1236	2	Q4P320_USTMA	Q4p320 ustilago ma	1401	77.5	4.4	1109	2	Q7NME3_GLOVI	Q7nme3 gloeobacter
1329	78	4.5	1242	2	Q9PZX3_EEEV	Q9pzx3 eastern equ	1402	77.5	4.4	1213	2	Q553Z2_DICDI	Q553z2 dictyosteli
1330	78	4.5	1303	2	Q76YA8_9CAUD	Q76ya8 bacterioph	1403	77.5	4.4	1234	1	CFAH_MOUSE	P06909 mus musculu
1331	78	4.5	1454	2	Q69A94_LEUME	Q69a94 leuconostoc	1404	77.5	4.4	1234	2	Q6NZK3_MOUSE	Q6nzk3 mus musculu
1332	78	4.5	1623	2	Q4SAP8_TETNG	Q4sap8 tetraodon n	1405	77.5	4.4	1258	1	ICEN_ENTAG	P16239 enterobacte
1333	78	4.5	1902	2	Q9Y878_COCPO	Q9y878 coccidioid	1406	77.5	4.4	1297	1	INSRR_HUMAN	P14616 homo sapien
1334	78	4.5	1963	2	Q9LXT9_ARATH	Q9lxt9 arabidopsis	1407	77.5	4.4	1297	2	Q5VZS3_HUMAN	Q5vzs3 homo sapien
1335	78	4.5	2261	2	Q61V05_CAEBR	Q61v05 caenorhabdi	1408	77.5	4.4	1359	2	Q6ESI7_ORYSA	Q6esi7 oryza sativ
1336	78	4.5	2261	2	Q4Q1Q2_LEIMA	Q4qlq2 leishmania	1409	77.5	4.4	1459	2	Q977Z6_THEVO	Q977z6 thermoplasm
1337	78	4.5	4370	2	Q9XSG8_PIG	Q9xsg8 sus scrofa	1410	77.5	4.4	1497	2	Q7USA4_RHOBA	Q7usa4 rhodopirell
1338	77.5	4.4	152	2	Q7Q217_ANOGA	Q7q217 anopheles g	1411	77.5	4.4	1656	2	Q5OSS7_ENTHI	Q5oss7 entamoeba h
1339	77.5	4.4	187	2	Q92531_HUMAN	Q92531 homo sapien	1412	77.5	4.4	1677	2	Q54CF9_DICDI	Q54cf9 dictyosteli
1340	77.5	4.4	189	1	ICYA_MANSE	P00305 manduca sex	1413	77.5	4.4	1706	2	Q8H6I0_MAIZE	Q8h6i0 zea mays (m
1341	77.5	4.4	197	2	Q8F122_LEPIN	Q8f122 leptospira	1414	77.5	4.4	2246	2	Q73C66_BACC1	Q73c66 bacillus ce
1342	77.5	4.4	206	1	ICYB_MANSE	Q00630 manduca sex	1415	77.5	4.4	2528	2	Q8AXP0_CYNPY	Q8axp0 cynops pyrr
1343	77.5	4.4	220	2	Q8H0L1_WHEAT	Q8h0l1 triticum ae	1416	77.5	4.4	2646	2	Q6XHA6_DICDI	Q6xha6 dictyosteli
1344	77.5	4.4	237	2	O69357_RHOER	O69357 rhodococcu	1417	77.5	4.4	3016	2	P73590_SYNY3	P73590 synechocyst
1345	77.5	4.4	250	2	Q5FWN8_XENLA	Q5fwn8 xenopus lae	1418	77	4.4	240	1	XYNC_STRLI	P26220 streptomyce

1492	77	4.4	917	2	Q9FLT8_ARATH	Q9flt8	arabidopsi
1493	77	4.4	1016	2	Q4S3H9_TETNG	Q4s3h9	tetraodon r
1494	77	4.4	1090	2	Q8A8I2_BACTN	Q8a8i2	bacteroides
1495	77	4.4	1110	2	Q8A894_BACTN	Q8a894	bacteroides
1496	77	4.4	1214	2	Q88193_9CALI	Q88193	san miguel
1497	77	4.4	1245	2	Q9Y7V5_TRIHA	Q9y7v5	trichoderma
1498	77	4.4	1358	1	PUR4_YEAST	P38972	saccharomyc
1499	77	4.4	1632	2	Q8TI41_METAC	Q8ti41	methanosarc
1500	77	4.4	1809	2	Q8T398_CIOIN	Q8t398	ciona intes
ALIGNMENTS							
RESULT 1							
Q5IWS5_HUMAN							
ID	Q5IWS5	HUMAN	PRELIMINARY;	PRT;	313	AA.	
AC	Q5IWS5;						
DT	10-MAY-2005	(TrEMBLrel. 30, Created)					
DT	10-MAY-2005	(TrEMBLrel. 30, Last sequence update)					
DT	10-MAY-2005	(TrEMBLrel. 30, Last annotation update)					
DE	Intelectin 1 (Intelectin variant).						
GN	Name=ITLN1;						
OS	Homo sapiens (Human).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;						
OC	Homo.						
OX	NCBI_TaxID=9606;						
RN	[1]						
RP	NUCLEOTIDE SEQUENCE.						
RC	TISSUE=Ovary;						
RA	Peavy T.R., Hedrick J.L.;						
RT	"Human homolog of the Xenopus laevis egg cortical granule lectin.";						
RL	Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.						
RN	[2]						
RP	NUCLEOTIDE SEQUENCE.						
RC	TISSUE=Adipose tissue;						
RA	Maruyama K., Sugano S.;						
RT	"Oligo-capping : a simple method to replace the cap structure of eucaryotic mRNAs with oligoribonucleotides.";						
RL	Gene 138:171-174(1994).						
RN	[3]						
RP	NUCLEOTIDE SEQUENCE.						
RC	TISSUE=Adipose tissue;						
RA	Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;						
RT	"Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library.";						
RL	Gene 200:149-156(1997).						
RN	[4]						
RP	NUCLEOTIDE SEQUENCE.						
RC	TISSUE=Adipose tissue;						
RA	Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;						
RL	Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.						
DR	EMBL; AY619691; AAU88047.1; -; mRNA.						
DR	EMBL; AK222533; BAD96253.1; -; mRNA.						
SQ	SEQUENCE 313 AA; 34977 MW; D82D4C173ED1B2EB CRC64;						
Query Match 100.0%; Score 1747; DB 2; Length 313;							
Best Local Similarity 100.0%; Pred. No. 3.1e-136;							
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Qy	1	MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSPDGLYFLRT	60				
Db	1	MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSPDGLYFLRT	60				
Qy	61	ENGVIYQTCDMTSGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANY	120				
Db	61	ENGVIYQTCDMTSGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANY	120				
Qy	121	NTFGSAEATSDDYKNPGYDIOAKDLGIWHVPNKSPMQHWNRSSLLRYRTDTGFLQTLG	180				
Db	121	NTFGSAEATSDDYKNPGYDIOAKDLGIWHVPNKSPMQHWNRSSLLRYRTDTGFLQTLG	180				





RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.";  
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
CC -!- FUNCTION: May play a role in the defense system against  
CC microorganisms. May specifically recognize carbohydrate chains of  
CC pathogens and bacterial components containing galactofuranosyl  
CC residues, in a calcium-dependent manner. May be involved in iron  
CC metabolism.  
CC -!- SUBUNIT: Homotrimer; disulfide-linked.  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
CC Also secreted.  
CC -!- TISSUE SPECIFICITY: Specifically expressed in the small intestine.  
CC Also found the heart, testis, colon, salivary gland, skeletal  
CC muscle, pancreas and thyroid; and to a lesser degree in the  
CC uterus, spleen, prostate, lymph node and thymus.  
CC -!- DEVELOPMENTAL STAGE: Found in fetal small intestine and thymus.  
CC -!- PTM: N-glycosylated.  
CC -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.  
CC -!- CAUTION: The two mouse genes Itln1a and Itln1b are the paralogs of  
CC human ITLN1.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
DR EMBL; AB036706; BAA96094.1; -; mRNA.  
DR EMBL; AF271386; AAM20741.1; -; mRNA.  
DR EMBL; AY065972; AAL58073.1; -; mRNA.  
DR EMBL; AY157361; AAO17800.1; -; mRNA.  
DR EMBL; AY157362; AAO17801.1; -; mRNA.  
DR EMBL; AY549722; AAS49907.1; -; mRNA.  
DR EMBL; CR457224; CAG33505.1; -; mRNA.  
DR EMBL; AY358359; AAQ88725.1; -; mRNA.  
DR EMBL; AK000029; BAA90893.1; -; mRNA.  
DR EMBL; BC020664; AAH20664.1; -; mRNA.  
DR Ensembl; ENSG00000179914; Homo sapiens.  
DR HGNC; HGNC:18259; ITLN1.  
DR InterPro; IPR002181; Fibrinogen\_C.  
DR Pfam; PF00147; Fibrinogen\_C; 1.  
DR SMART; SM00186; FBG; 1.  
DR PROSITE; PS00514; FIBRIN\_AG\_C\_DOMAIN; FALSE NEG.  
KW Direct protein sequencing; Glycoprotein; GPI-anchor; Lectin;  
KW Lipoprotein; Membrane; Polymorphism; Signal.  
FT SIGNAL 1 18  
FT CHAIN 19 298 Intelectin-1.  
FT PROPEP 299 313 Potential.  
FT DOMAIN 36 209 Fibrinogen C-terminal.  
FT LIPID 298 298 GPI-anchor amidated serine (Potential).  
FT CARBOHYD 163 163 N-linked (GlcNAc...) (Probable).  
FT VARIANT 109 109 V -> D (in dbSNP:2274907).  
FT VARIANT 313 313 R -> P (in dbSNP:8144).  
FT SEQUENCE 313 AA; 34962 MW; 56219FE937FC802E CRC64;  
SQ  
Query Match 99.5%; Score 1738; DB 1; Length 313;  
Best Local Similarity 99.7%; Pred. No. 1.7e-135;  
Matches 312; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MNQLSFLFLIATTRGWSSTDEANTYFKWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 60  
Db 1 MNQLSFLFLIATTRGWSSTDEANTYFKWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 60  
Qy 61 ENGVIYQTFCDMTSGGGGWTLLVASVHENDMRGKCTVGDWRSSQQGSKADYPEGDGNWANY 120  
Db 61 ENGVIYQTFCDMTSGGGGWTLLVASVHENDMRGKCTVGDWRSSQQGSKAVYPEGDGNWANY 120  
Qy 121 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMOHWRNSSLLRYRTDTGFLQTLG 180  
Db 121 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMOHWRNSSLLRYRTDTGFLQTLG 180  
Qy 181 HNLFGIYQKYPVKYGEGKCTWDNGPVPVVDYFGDAQKTASYSPYQREFTAGFVQFRV 240  
Db 181 HNLFGIYQKYPVKYGEGKCTWDNGPVPVVDYFGDAQKTASYSPYQREFTAGFVQFRV 240  
Qy 241 FNNEAANALCAGMRVTGCNTEHHICIGGGYFFPEASPOCCGDFSGDFWSGYGTHVGYS 300  
Db 241 FNNEAANALCAGMRVTGCNTEHHICIGGGYFFPEASPOCCGDFSGDFWSGYGTHVGYS 300  
Qy 301 REITEAAVLLFYR 313  
Db 301 REITEAAVLLFYR 313  
RESULT 4  
Q5IWS4 HUMAN  
ID Q5IWS4\_HUMAN PRELIMINARY; PRT; 313 AA.  
AC Q5IWS4;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DE Intelectin 1.  
GN Name=ITLN1;

Qy 181 HNLFGIYQKYPVKYGEGKCTWDNGPVPVVDYFGDAQKTASYSPYQREFTAGFVQFRV 240  
Db 181 HNLFGIYQKYPVKYGEGKCTWDNGPVPVVDYFGDAQKTASYSPYQREFTAGFVQFRV 240  
Qy 241 FNNEAANALCAGMRVTGCNTEHHICIGGGYFFPEASPOCCGDFSGDFWSGYGTHVGYS 300  
Db 241 FNNEAANALCAGMRVTGCNTEHHICIGGGYFFPEASPOCCGDFSGDFWSGYGTHVGYS 300  
Qy 301 REITEAAVLLFYR 313  
Db 301 REITEAAVLLFYR 313  
RESULT 3  
Q5VYI4 HUMAN  
ID Q5VYI4\_HUMAN PRELIMINARY; PRT; 313 AA.  
AC Q5VYI4;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Intelectin 1 (Galactofuranose binding).  
GN Name=ITLN1; ORFNames=RP11-312J18.4-001;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Van Hellmond Z.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL354714; CAH72357.1; -; Genomic DNA.  
SQ SEQUENCE 313 AA; 34961 MW; 56219FE937FC802E CRC64;  
Query Match 99.5%; Score 1738; DB 2; Length 313;  
Best Local Similarity 99.7%; Pred. No. 1.7e-135;  
Matches 312; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MNQLSFLFLIATTRGWSSTDEANTYFKWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 60  
Db 1 MNQLSFLFLIATTRGWSSTDEANTYFKWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 60  
Qy 61 ENGVIYQTFCDMTSGGGGWTLLVASVHENDMRGKCTVGDWRSSQQGSKADYPEGDGNWANY 120  
Db 61 ENGVIYQTFCDMTSGGGGWTLLVASVHENDMRGKCTVGDWRSSQQGSKAVYPEGDGNWANY 120  
Qy 121 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMOHWRNSSLLRYRTDTGFLQTLG 180  
Db 121 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMOHWRNSSLLRYRTDTGFLQTLG 180  
Qy 181 HNLFGIYQKYPVKYGEGKCTWDNGPVPVVDYFGDAQKTASYSPYQREFTAGFVQFRV 240  
Db 181 HNLFGIYQKYPVKYGEGKCTWDNGPVPVVDYFGDAQKTASYSPYQREFTAGFVQFRV 240  
Qy 241 FNNEAANALCAGMRVTGCNTEHHICIGGGYFFPEASPOCCGDFSGDFWSGYGTHVGYS 300  
Db 241 FNNEAANALCAGMRVTGCNTEHHICIGGGYFFPEASPOCCGDFSGDFWSGYGTHVGYS 300  
Qy 301 REITEAAVLLFYR 313  
Db 301 REITEAAVLLFYR 313  
RESULT 4  
Q5IWS4 HUMAN  
ID Q5IWS4\_HUMAN PRELIMINARY; PRT; 313 AA.  
AC Q5IWS4;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DE Intelectin 1.  
GN Name=ITLN1;





OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;	
OC	Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RA	Van Hellmond Z.;	
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.	
RN	[2]	
RP	NUCLEOTIDE SEQUENCE.	
RA	Harrison E.;	
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AL354714; CAH72351.1; -; Genomic DNA.	
DR	EMBL; AL591806; CAI15364.1; -; Genomic DNA.	
DR	EMBL; AL591806; CAH72351.1; JOINED; Genomic DNA.	
DR	EMBL; AL354714; CAI15364.1; JOINED; Genomic DNA.	
SQ	SEQUENCE 325 AA; 36211 MW; 283C9A12AED2EBFC CRC64;	
	Query Match 83.0%; Score 1449.5; DB 2; Length 325;	
	Best Local Similarity 83.0%; Pred. No. 1.3e-111;	
	Matches 264; Conservative 18; Mismatches 31; Indels 5; Gaps 3;	
Qy	1 MNQLSFLFLIATTRGWSDEANT--YFKEW-TCS-SSPSLPRSCKEIKDECPSAFDGL 55	
Db	8 MTRLCLFLFFSVATSGCSAAAASSLEMLSRPFETCAFSFSLPRSCKEIKERCHSAGDGL 67	
Qy	56 YFLRTENGVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSQQGSKADYPEGDG 115	
Db	68 YFLRTKNGVVYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSQQGKNKADYPEGDG 127	
Qy	116 NWANYNTFGSBAATSDDYKNPGYYDIOAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGF 175	
Db	128 NWANYNTFGSBAATSDDYKNPGYYDIOAKDLGIWHVPNKSPMQHWRNSALLRYRTNTGF 187	
Qy	176 LQTLGHNLFGIYQKYPVKYGEKCKWTNNGVPIVVYDFGDAQKTASYSPYQREFTAGF 235	
Db	188 LQRLGHNLFGIYQKYPVKYRSGKWNNGPAIPVVYDFGDAKKTASYSPYQREFVAGF 247	
Qy	236 VQFRVFNNERAAALCAGMRVTGCNTEHHICGGGYFPPEASPOQCQGFSGFDWSGYGTHV 295	
Db	248 VQFRVFNNERAAALCAGIKVTGCNTEHHICGGGFFPQGPQKPRQCQGFSAFDWDGYGTHV 307	
Qy	296 GYSSSREITEAAVLLFYR 313	
Db	308 KSSCSREITEAAVLLFYR 325	
RESULT 7		
ITL1A MOUSE		
ID	ITL1A MOUSE STANDARD; PRT; 313 AA.	
AC	O88310;	
DT	01-FEB-2005 (Rel. 46, Created)	
DT	01-FEB-2005 (Rel. 46, Last sequence update)	
DT	13-SEP-2005 (Rel. 48, Last annotation update)	
DE	Intelectin-1a precursor (Intestinal lactoferrin receptor)	
DE	(Galactofuranose binding lectin).	
GN	Name=Itln1a; Synonyms=Int1, Itln, Itina;	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;	
OC	Muroidea; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE, FUNCTION, AND TISSUE SPECIFICITY.	
RC	STRAIN=BALB/c; TISSUE=Intestine;	
RX	MEDLINE=99008898; PubMed=9790983; DOI=10.1006/bbrc.1998.9513;	
RA	Komiya T., Tanigawa Y., Hirohashi S.;	
RT	"Cloning of the novel gene intelectin, which is expressed in	
RT	intestinal Paneth cells in mice.";	
RL	Biochem. Biophys. Res. Commun. 251:759-762(1998).	
RN	[2]	
RP	NUCLEOTIDE SEQUENCE.	

RC	STRAIN=C57BL/6J, and FVB/N; TISSUE=Intestine, and Thymus;	
RX	PubMed=14720597; DOI=10.1016/S1095-6433(03)00269-1;	
RA	Chang B.Y., Peavy T.R., Wardrip N.J., Hedrick J.L.;	
RT	"The Xenopus laevis cortical granule lectin: cDNA cloning,	
RT	developmental expression, and identification of the eglectin family of	
RT	lectins.";	
RL	Comp. Biochem. Physiol. 137A:115-129(2004).	
RN	[3]	
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].	
RX	PubMed=12466851; DOI=10.1038/nature01266;	
RA	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,	
RA	Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,	
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,	
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,	
RA	Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,	
RA	Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,	
RA	Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,	
RA	Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,	
RA	Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,	
RA	Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,	
RA	Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,	
RA	Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,	
RA	Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,	
RA	Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,	
RA	Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,	
RA	Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,	
RA	Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,	
RA	Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,	
RA	Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,	
RA	Huan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,	
RA	Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,	
RA	Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,	
RA	Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,	
RA	Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,	
RA	Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,	
RA	Birney E., Hayashizaki Y.;	
RT	"Analysis of the mouse transcriptome based on functional annotation of	
RT	60,770 full-length cDNAs.";	
RL	Nature 420:563-573(2002).	
RN	[4]	
RP	TISSUE SPECIFICITY.	
RC	STRAIN=BALB/c; TISSUE=Intestine;	
RX	PubMed=15265922; DOI=10.173/3/1894;	
RA	Pemberton A.D., Knight P.A., Gamble J., Colledge W.H., Lee J.K.,	
RA	Pierce M., Miller H.R.;	
RT	"Innate BALB/c enteric epithelial responses to Trichinella spiralis:	
RT	inducible expression of a novel goblet cell lectin, intelectin-2, and	
RT	its natural deletion in C57BL/10 mice.";	
RL	J. Immunol. 173:1894-1901(2004).	
CC	-!- FUNCTION: May play a role in the defense system against	
CC	microorganisms. May specifically recognize carbohydrate chains of	
CC	pathogens and bacterial components containing galactofuranosyl	
CC	residues, in a calcium-dependent manner. May be involved in iron	
CC	metabolism (By similarity).	
CC	-!- SUBUNIT: Homotrimer; disulfide-linked (By similarity).	
CC	-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.	
CC	Also secreted (By similarity).	
CC	-!- TISSUE SPECIFICITY: Expressed in small intestinal Paneth cells in	
CC	uninfected mice.	
CC	-!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.	
CC	-!- CAUTION: The two mouse genes Itln1a and Itln1b are the paralogs of	
CC	human ITLN1.	
CC	-----	
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use as long as its content is in no way modified and this statement is not	
CC	removed.	
CC	-----	
DR	EMBL; AB016496; BAA31992.1; -; mRNA.	
DR	EMBL; AY157363; AAO17802.1; -; mRNA.	
DR	EMBL; AY157364; AAO17803.1; -; mRNA.	
DR	EMBL; AK007447; BAB25043.1; -; mRNA.	

DR PIR; JE0328; JE0328.  
DR Ensembl; ENSMUSG00000038209; Mus musculus.  
DR MGI; MGI:1333831; Itlna.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0009624; P:response to nematodes; IDA.  
DR InterPro; IPR002181; Fibrinogen C.  
DR Pfam; PF00147; Fibrinogen\_C; 1.  
DR SMART; SM00186; FBG; 1.  
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; FALSE NEG.  
KW GPI-anchor; Lectin; Lipoprotein; Membrane; Signal.  
FT SIGNAL 1 19 By similarity.  
FT CHAIN 20 298 Intelectin-1a.  
FT PROPEP 299 313 Potential.  
FT DOMAIN 36 211 Fibrinogen C-terminal.  
FT LIPID 298 298 GPI-anchor amidated serine (Potential).  
SQ SEQUENCE 313 AA; 34953 MW; D2FA447D3D8547A4 CRC64;

Query Match  
Best Local Similarity 81.7%; Score 1427; DB 1; Length 313;  
Matches 255; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

QY 1 MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 60  
Db 1 MTQLGFLLFIMVATRGCSAAEENLDNRWGNSEFFSSLPSCKEIKQEHTKAQDGLYFLRT 60

QY 61 ENGVIYQTFCDMTSGGGWTLVASVHENDMRGKCTVGDWSSQQGSKADYPEGDGNWANY 120  
Db 61 KNGVIYQTFCDMTTAGGGWTLVASVHENNMKGCTVGDWSSQQGNRADYPEGDGNWANY 120

QY 121 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG 180  
Db 121 NTFGSAEAATSDDYKNPGYFDIQAENLGIWHVPNKSPHLNWRKSSLLRYRTFTGFLQHLG 180

QY 181 HNLFGIYQKYPVKYGEKCKWTDNGPVPVYVDFGDAQKTASYSPYQGREFTAGVQFRV 240  
Db 181 HNLFGIYQKYPVKYGEKCKWTDNGPALPVYVDFGDARKTASYSPSGQREFTAGVQFRV 240

QY 241 FNNERAANALCAGMRVTGCTEHHICIGGGYFPEASPOCGDFSGFDMWSGYGTHVGYS 300  
Db 241 FNNERAASALCAGRVVTCNTEHHICIGGGFFPEGNPVQCGDFASFDWDGYGTHNGYSS 300

QY 301 REITEAAVLLFYR 313  
Db 301 RKITEAAVLLFYR 313

RESULT 8  
Q5IWS3\_MOUSE PRELIMINARY; PRT; 313 AA.  
AC Q5IWS3;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Intelectin 1.  
GN Name=Itlna; Synonyms=Itln1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=NIH Swiss; TISSUE=Ovary;  
RX Peavy T.R., Hedrick J.L.;  
RT "Mouse homolog of the Xenopus laevis egg cortical granule lectin.";  
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY619693; AAU88049.1; -; mRNA.  
DR MGI; MGI:1333831; Itlna.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0009624; P:response to nematodes; IDA.  
SQ SEQUENCE 313 AA; 34953 MW; D2FA447D3D8547A4 CRC64;

Query Match  
81.7%; Score 1427; DB 2; Length 313;

Best Local Similarity 81.5%; Pred. No. 9.3e-110;  
Matches 255; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

QY 1 MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 60  
Db 1 MTQLGFLLFIMVATRGCSAAEENLDNRWGNSEFFSSLPSCKEIKQEHTKAQDGLYFLRT 60

QY 61 ENGVIYQTFCDMTSGGGWTLVASVHENDMRGKCTVGDWSSQQGSKADYPEGDGNWANY 120  
Db 61 KNGVIYQTFCDMTTAGGGWTLVASVHENNMKGCTVGDWSSQQGNRADYPEGDGNWANY 120

QY 121 NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG 180  
Db 121 NTFGSAEAATSDDYKNPGYFDIQAENLGIWHVPNKSPHLNWRKSSLLRYRTFTGFLQHLG 180

QY 181 HNLFGIYQKYPVKYGEKCKWTDNGPVPVYVDFGDAQKTASYSPYQGREFTAGVQFRV 240  
Db 181 HNLFGIYQKYPVKYGEKCKWTDNGPALPVYVDFGDARKTASYSPSGQREFTAGVQFRV 240

QY 241 FNNERAANALCAGMRVTGCTEHHICIGGGYFPEASPOCGDFSGFDMWSGYGTHVGYS 300  
Db 241 FNNERAASALCAGRVVTCNTEHHICIGGGFFPEGNPVQCGDFASFDWDGYGTHNGYSS 300

QY 301 REITEAAVLLFYR 313  
Db 301 RKITEAAVLLFYR 313

RESULT 9  
ITL1B\_MOUSE  
ID ITL1B\_MOUSE STANDARD; PRT; 313 AA.  
AC Q80ZA0;  
DT 01-FEB-2005 (Rel. 46, Created)  
DT 01-FEB-2005 (Rel. 46, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Intelectin-1b precursor (Intelectin-2).  
GN Name=Itlnb; Synonyms=Itln2, Itlnb;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=BALB/c; TISSUE=Intestine;  
RX PubMed=15265922; DOI=173/3/1894;  
RA Pemberton A.D., Knight P.A., Gamble J., Colledge W.H., Lee J.K.,  
RA Pierce M., Millier H.R.;  
RT "Innate BALB/c enteric epithelial responses to Trichinella spiralis:  
RT inducible expression of a novel goblet cell lectin, intelectin-2, and  
RT its natural deletion in C57BL/10 mice.";  
RL J. Immunol. 173:1894-1901(2004).  
CC -!- FUNCTION: May play a protective role in the innate immune response  
CC to parasite infection.  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
CC Also secreted (By similarity).  
CC -!- TISSUE SPECIFICITY: Expressed in the globlet and Paneth cell of  
CC small intestine of infected mice. Expressed in the ileum of  
CC uninfected mice.  
CC -!- INDUCTION: Up-regulated early (day 3) during infection with  
CC parasite and level remained high through to day 14, time of  
CC parasite rejection.  
CC -!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.  
CC -!- CAUTION: The two mouse genes Itlna and Itlnb are the paralogs of  
CC human ITLN1.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; AY217760; AAO60215.1; -; mRNA.

DR Ensembl; ENSMUSG00000038209; Mus musculus.  
DR MGI; MGI:3057189; Itlnb.  
DR InterPro; IPR002181; Fibrinogen\_C.  
DR Pfam; PF00147; Fibrinogen\_C; 1.  
DR SMART; SM00186; FBG; 1.  
DR PROSITE; PS00514; FIBRIN\_AG\_C DOMAIN; FALSE NEG.  
KW Glycoprotein; GPI-anchor; Lectin; Lipoprotein; Membrane; Signal.  
FT SIGNAL 1 19 Potential.  
FT CHAIN 20 298 Intelectin-1b.  
FT PROPEP 299 313 Potential.  
FT DOMAIN 36 209 Fibrinogen C-terminal.  
FT LIPID 298 298 GPI-anchor amidated serine (Potential).  
FT CARBOHYD 163 163 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 313 AA; 35070 MW; BEF4E2757C71FC00 CRC64;  
  
Query Match 79.6%; Score 1391; DB 1; Length 313;  
Best Local Similarity 79.6%; Pred. No. 8.9e-107;  
Matches 249; Conservative 24; Mismatches 40; Indels 0; Gaps 0;  
  
QY 1 MNQLSFLFLFIATTRGWSSTDEANTYFKWTCSSTSPSLPRSCKEIKDECPSAFDGLYFLRT 60  
Db 1 MTQLGLFLFIATTRVCSAAEENLDTNRWGSFFSSLPSCKEIKQEDTKAQDGLYFLRT 60  
  
QY 61 ENGVIYQTFCDMTSGGGWTLVASVHENDMRGKCTVGDWRSSQQGSKADYPEGDNWANY 120  
Db 61 ENGVIYQTFCDMTTAGGGWTLVASVHENNLGRCTVGDWRSSQQGNRADYPEGDNWANY 120  
  
QY 121 NTFGSABAATSDDYKNPGYYDIOAKDLGIWHVPKNSPMQHWNRNSSLRLRYRTDTGFLQTLG 180  
Db 121 NTFGSAEGATSDDYKNPGYFDIOAENLGIWHVPNNSPLHTWRNSSLRLRYRTFTGFLQRLG 180  
  
QY 181 HNLFGIYQKYPVKYGEKCKWTNDGNPVPVYVDFGDAQKTASYSPYQGREFTAGFVQFRV 240  
Db 181 HNLFGLYQKYPVKYGEKCKWTNDGNPAFPVYVDFGDAQKTASYSPSGRNEFTAGYVQFRV 240  
  
QY 241 FNNERAANALCAGMRVTGCNTEHHCIGGGYFPPEASPOQCGDFSGFDMSGYGTHTVGYSSS 300  
Db 241 FNNERAASALCAGVRVTGCNTEHHCIGGGGFPEFDPEECGDFAAFDANGYGTHTIRYSNS 300  
  
QY 301 REITEAAVLLFYR 313  
Db 301 REITEAAVLLFYR 313  
  
RESULT 10  
Q6PY6\_XENTR PRELIMINARY; PRT; 339 AA.  
AC Q6PY6;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein MGC76330.  
GN Name=MGC76330;  
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus; Silurana.  
OX NCBI\_TaxID=8364;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RA Klein S., Gerhard D.S.;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC061445; AAH61445.1; -; mRNA.  
DR InterPro; IPR002181; Fibrinogen\_C.  
DR Pfam; PF00147; Fibrinogen\_C; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 339 AA; 37057 MW; 7E9DFDABA7EA441D CRC64;  
  
Query Match 64.6%; Score 1129; DB 2; Length 339;  
Best Local Similarity 66.7%; Pred. No. 4.7e-85;  
Matches 208; Conservative 29; Mismatches 65; Indels 10; Gaps 2;  
  
QY 7 LLFLIATTRGWSSTDEANTYFKWTCSSTSPSLP-----RSCKEIKDECPSAFDGLYFLRTE 61  
Db 33 ILNLLACWTEDKTDNSGRF-----SGSPTGDMSYGYRSCNEIKSSDPSAPDGIYTLATE 87  
  
QY 62 NGVIYQTFCDMTSGGGWTLVASVHENDMRGKCTVGDWRSSQQGSKADYPEGDNWANYN 121  
Db 88 HGESYQTFCDMTTGGGWTLLVASVHENNMFGKCTVGDWRSTQQGNTLQNPEGDNWANYA 147  
  
QY 122 TFGSAEAATSDDYKNPGYYDIOAKDLGIWHVPKNSPMQHWNRNSSLRLRYRTDTGFLQTLGH 181  
Db 148 TFGLPEGATSDDYKNPGYYDIOAKNLALWHVPNTPMFNWRNSSLRLRYRTQNSFTEEGG 207  
  
QY 182 NLFGIYQKYPVKYGEKCKWTNDGNPVPVYVDFGDAQKTASYSPYQGREFTAGFVQFRVF 241  
Db 208 NLFELYKYPVKYDIGKCLADNGPAVPVYVYDLGSAEKTSSLYSPNGRNEFTAGFVQFRVV 267  
  
QY 242 NNERRAANALCAGMRVTGCNTEHHCIGGGYFPPEASPOQCGDFSGFDMSGYGTHTVGYSSSR 301  
Db 268 NTEKAALALCPGVKVGKCNAAEHHCIGGGYFPPEGSPRQCGDFSAFDWDGYGTHAGWSASK 327  
  
QY 302 EITEAAVLLFYR 313  
Db 328 EITEAAVLLLYR 339  
  
RESULT 11  
Q8JJD0\_XENLA PRELIMINARY; PRT; 338 AA.  
AC Q8JJD0;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE 35 kDa serum lectin.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Ishino T., Sekimizu K., Natori S., Kubo T.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB061238; BAB91359.1; -; mRNA.  
DR GO; GO:0005529; F:sugar binding; IEA.  
DR GO; GO:0007596; P:blood coagulation; IEA.  
DR InterPro; IPR002181; Fibrinogen\_C.  
DR Pfam; PF00147; Fibrinogen\_C; 1.  
DR SMART; SM00186; FBG; 1.  
KW Lectin.





Query Match 62.7%; Score 1095; DB 2; Length 339;  
Best Local Similarity 60.9%; Pred. No. 3e-82;  
Matches 206; Conservative 34; Mismatches 70; Indels 28; Gaps 4;

QY 4 LSFLLFLIATT-----RGWSTDEANTYFKE-----WT-----CSSPSLP----- 38  
Db 2 LSYSLLLALLAFPAHGAGSCEQASISEKKEKILNLLACWTEGNADNSLSRSGSPTGDMN 61

QY 39 ---RSCKEIKDECPSAFDGLYFLRTENGVIYQTFCDMTSGGGWTLVASVHENDMRGKCT 95  
Db 62 YGYRSCNEIKSSSRAPDGIYTLATEDGESYQTFCDMTTNGGWTTLVASVHENNMFCKT 121

QY 96 VGDWRSSQQGSKADYPEGDNWANYNTFGSAEAATSDDYKNPGYYDIAQKDLGIWHVPNK 155  
Db 122 VGDWRSTQQGNMLQNPEGDNWANYATFGLPEGATSDDYKNPGYYDIEAKNLALWHVPNK 181

QY 156 SPMQHWRNSSLLRYRTDTGFLQTLGHNLFGLIYQKYPVKYGEKGCWTDNGPVIWVYDFGD 215  
Db 182 TPMVMWRNSSILRYRTQNGFLTTEEGNLFELYKYPVKYDYGKCLADNGPAVPVYDLGS 241

QY 216 AQKTASYSPYQREFTAGFVQFRVFNNERAANALCAGMRVTGCNTEHHICIGGGYFPEA 275  
Db 242 AEKTASLYSPNGRSEFTPGFVQFRAVNSERATLALCAGVKVGCNVEHHICIGGGYIPEG 301

QY 276 SPQCCGDFSGFDSGYGTHVGYSSSREITEAAVLLFYR 313  
Db 302 SPROCGDFAALDWDGYGTNLGWSASKQIIIEAAVMLFYR 339

RESULT 14  
Q8JJC9\_XENLA  
ID Q8JJC9\_XENLA PRELIMINARY; PRT; 315 AA.  
AC Q8JJC9;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Lectin type 2.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Ishino T., Sekimizu K., Natori S., Kubo T.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB061239; BAB91360.1; -; mRNA.  
DR GO; GO:0007596; P:blood coagulation; IEA.  
DR InterPro; IPR002181; Fibrinogen\_C.  
DR Pfam; PF00147; Fibrinogen\_C; 1.  
DR SMART; SM00186; FBG; 1.  
SQ SEQUENCE 315 AA; 34329 MW; 515C3C6F7F12B69A CRC64;

Query Match 61.8%; Score 1080; DB 2; Length 315;  
Best Local Similarity 63.7%; Pred. No. 4.8e-81;  
Matches 198; Conservative 33; Mismatches 78; Indels 2; Gaps 1;

QY 5 SFLLFLIATTRGWSDEANTYFKEWT--CSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN 62  
Db 5 SLLLVVLIFTGTCRTEPFSLHFEPYPTGGTSSNGFSRNCKEIKDSDSAKDGIYNLITAN 64

QY 63 GVIYQTFCDMTSGGGWTLVASVHENDMRGKCTVGDWRSSQQGSKADYPEGDNWANYNT 122  
Db 65 GETYQAFCDMTTDDGGWTLVASVHENNMFCKTVGDWRSSQQGNINNPEGGNWANYAT 124

QY 123 FGSAAEAATSDDYKNPGYYDIAQKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGTGFLQTLGHN 182  
Db 125 FGLPEGATGDDYKNPGYYDISAKOLAIWHVFNNTPMTSWRSSLLRYRTSNGFFPSEGGN 184

QY 183 LFGIYQKYPVKYGEKGCWTDNGPVIWVYDFGDAQKTASYSPYQREFTAGFVQFRVN 242  
Db 185 LFNLYKKYPVIYNTGSCQTNNGPAVPVLYDFGDPKTTSMYSPNGRGEFIAGFVQFRVN 244

QY 243 NERAANALCAGMRVTGCNTEHHICIGGGYFPEASPOCCGDFSGFDSGYGTHVGYSSRE 302  
Db 245 TERAPLALCPGIKVTGCNAEHHICIGGGFIPEGNPVQCGDFAAFDWNMGYGTGYAWSSTKA 304

QY 303 ITEAAVLLFYR 313  
Db 305 ITEAAVLLMYR 315

RESULT 15  
Q91719\_XENLA  
ID Q91719\_XENLA PRELIMINARY; PRT; 313 AA.  
AC Q91719;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Cortical granule lectin.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Ovary;  
RA Chang B.Y., Wardrip N.J., Hedrick J.L.;  
RT "Molecular cloning and characterization of cortical granule lectin: an  
RT essential glycoprotein involved in the block of polyspermy.";  
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Ovary;  
RA Hedrick J.L.;  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X82626; CAA57946.1; -; mRNA.  
DR PIR; S49589; S49589.  
DR GO; GO:0005529; F:sugar binding; IEA.  
DR GO; GO:0007596; P:blood coagulation; IEA.  
DR InterPro; IPR002181; Fibrinogen\_C.  
DR SMART; SM00186; FBG; 1.  
KW Lectin.  
FT CHAIN 16 313 Potential.  
SQ SEQUENCE 313 AA; 34304 MW; 519762656E82507E CRC64;

Query Match 60.1%; Score 1049.5; DB 2; Length 313;  
Best Local Similarity 61.5%; Pred. No. 1.6e-78;  
Matches 192; Conservative 37; Mismatches 72; Indels 11; Gaps 2;

QY 8 LFLIATTRGWSTD-----EANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 60  
Db 5 ILLLLVTGSLQSCEPVVIVASKNMVKQLDCDKF----RSCKEIKDSNEEAQDGIYTLTS 60

QY 61 ENGVIYQTFCDMTSGGGWTLVASVHENDMRGKCTVGDWRSSQQGSKADYPEGDNWANY 120  
Db 61 SDGISYQTFCDMTTNGGWTTLVASVHENNMGAKCTIGDRWSSQQGNRADYPEGDNWANY 120

QY 121 NTFGSAAEAATSDDYKNPGYYDIAQKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGTGFLQTLG 180  
Db 121 NTFGSAGGATSDDYKNPGYYDIEAYNLGVHWHPNKTPLSVWRNSSLQRYRTTGDILFKHG 180

QY 181 HNLFGIYQKYPVKYGEKGCWTDNGPVIWVYDFGDAQKTASYSPYQREFTAGFVQFRV 240  
Db 181 GNLFSLYRIYPVKYIGIGSCSKDSGPTVPVWYDLGSAKLITASFISPDFRSQFTPGYIQFRP 240

QY 241 FNNERAANALCAGMRVTGCNTEHHICIGGGYFPEASPOCCGDFSGFDSGYGTHVGYSSS 300  
Db 241 INTEKAALALCPGMKMWESCNVHVCIGGGGYFPEADPRQCQDFAAYDFNGYGTKKFNSAG 300

QY 301 REITEAAVLLFY 312  
Db 301 IEITEAAVLLFY 312

Thu Feb 9 11:59:17 2006

us-10-063-595-88.multi.rup

Page 20

Search completed: February 8, 2006, 19:42:23  
Job time : 307 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 8, 2006, 19:37:48 ; Search time 43 Seconds  
(without alignments)  
700.369 Million cell updates/sec

Title: US-10-063-595-88  
Perfect score: 1747  
Sequence: 1 MNQLSFLLPLIATTRGWSTD.....HVGYSRSSREITEAAVLLPYR 313

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1427	81.7	313	2 JE0328	intellectin - mouse
2	866.5	49.6	302	2 S49589	cortical granule 1
3	129.5	7.4	282	2 A35084	fibrinogen-related
4	109	6.2	491	1 FGHUB	fibrinogen beta ch
5	107.5	6.2	1045	2 S23570	pol polyprotein ho
6	105.5	6.0	189	2 C81428	peptidyl-prolyl ci
7	105.5	6.0	616	2 T32131	hypothetical prote
8	100	5.7	2265	1 FNBO	fibrinectin - bovi
9	99	5.7	328	2 A05299	fibrinogen beta ch
10	99	5.7	444	2 S05313	fibrinogen gamma-B
11	99	5.7	796	1 JV0107	glucose dehydrogen
12	99	5.7	796	2 H85495	glucose dehydrogen
13	99	5.7	796	2 H90644	glucose dehydrogen
14	98.5	5.6	725	2 H81030	TonB-dependent rec
15	97	5.6	496	1 A46725	omega-crystallin -
16	95.5	5.5	450	2 S38114	hypothetical prote
17	95.5	5.5	463	2 A38463	fibrinogen beta ch
18	95.5	5.5	479	2 A25052	fibrinogen beta ch
19	95	5.4	725	2 D81976	probable ferric si
20	94.5	5.4	649	2 D90496	hypothetical prote
21	94	5.4	1018	2 AG2556	hypothetical prote
22	93.5	5.4	551	1 A31389	beta-amylase (EC 3
23	93	5.3	468	1 FGBOB	fibrinogen beta ch
24	92.5	5.3	1332	2 T23024	hypothetical prote
25	92	5.3	796	2 AG0523	glucose dehydrogen
26	91	5.2	493	2 JC8027	type 1 angiotensin
27	90	5.2	2201	2 A32160	tenascin-C - human
28	89.5	5.1	600	2 I49281	fertilin alpha pre
29	89.5	5.1	1054	2 T18304	acid trehalase hom

30	89.5	5.1	1810	1 A32230	tenascin precursor
31	89	5.1	326	2 S61517	ficolin-1 precursor
32	89	5.1	798	2 S20881	homeotic protein p
33	89	5.1	2351	2 G71415	hypothetical prote
34	88	5.0	243	2 T28802	hypothetical prote
35	88	5.0	337	2 S55932	NCA3 protein precu
36	88	5.0	687	2 AG0495	alpha-amylase (EC
37	88	5.0	964	2 S51324	pullulanase - spin
38	88	5.0	1914	2 T42635	tenascin Y precurs
39	87.5	5.0	839	2 E84824	hypothetical prote
40	87.5	5.0	913	2 G64110	hypothetical prote
41	87.5	5.0	2817	2 B97033	uncharacterized pr
42	87	5.0	361	2 JN0716	glutamate-ammonia
43	87	5.0	426	1 BVECID	lysine 6-monooxyge
44	87	5.0	545	2 F86834	alpha-glucosidase
45	87	5.0	646	2 S66863	hypothetical prote
46	86.5	5.0	334	2 JC5980	ficolin-A precursor
47	86.5	5.0	641	2 T07668	starch synthase (E
48	86.5	5.0	2555	2 A40043	notch protein homo
49	86	4.9	564	1 HMIVF9	hemagglutinin prec
50	86	4.9	1356	2 A45445	janusin precursor,
51	85.5	4.9	866	2 D44234	fibrinogen alpha c
52	85.5	4.9	1806	1 CGHUIE	collagen alpha 1(X
53	85.5	4.9	1843	2 S18803	collagen alpha 1(V
54	85	4.9	349	2 F84246	hypothetical prote
55	85	4.9	764	2 A72394	alpha-xylosidase -
56	85	4.9	6669	2 S55024	nebulin, skeletal
57	84.5	4.8	610	2 JH0573	chitinase (EC 3.2.
58	84.5	4.8	2175	1 GNNYBE	genome polyprotein
59	84	4.8	420	2 JC2249	pectate lyase (EC
60	84	4.8	420	2 S39459	pectate lyase (EC
61	84	4.8	463	2 T15876	hypothetical prote
62	84	4.8	551	2 S05667	glucan 1,4-alpha-m
63	83.5	4.8	308	2 T29756	hypothetical prote
64	83.5	4.8	500	1 A23874	nitrogenase (EC 1.
65	83.5	4.8	688	2 H96681	protein F1E22.10 [
66	83.5	4.8	702	2 T13505	NADH2 dehydrogenas
67	83	4.8	363	2 T25278	hypothetical prote
68	83	4.8	501	2 T05640	histone deacetylas
69	83	4.8	553	2 B72863	HE65 protein - Aut
70	83	4.8	1309	2 T00078	probable RNA-direc
71	83	4.8	2019	1 JQ1322	tenascin precursor
72	83	4.8	2386	1 FNHU	fibrinectin precur
73	82.5	4.7	312	2 JN0596	fibrinogen-related
74	82.5	4.7	405	2 T40300	histone deacetylas
75	82.5	4.7	455	2 A86306	F20D23.27 protein
76	82.5	4.7	609	2 T42073	probable chitinase
77	82.5	4.7	698	2 D90771	hypothetical prote
78	82.5	4.7	698	2 H85633	hypothetical prote
79	82.5	4.7	840	2 A87639	TonB-dependent rec
80	82.5	4.7	1161	2 D83076	type 4 fimbrial bi
81	82.5	4.7	1254	1 JQ1979	structural polypro
82	82.5	4.7	4135	2 T42629	tenascin-X - bovin
83	82	4.7	220	2 S28170	tenascin homolog -
84	82	4.7	363	2 AE0616	outer membrane pro
85	82	4.7	363	2 S43159	outer membrane por
86	82	4.7	373	1 AJCHQ	glutamate-ammonia
87	82	4.7	417	2 S65944	tenascin-X - pig (
88	82	4.7	463	2 A48375	cellulase (EC 3.2.
89	82	4.7	478	2 JN0892	metalloprotease
90	82	4.7	593	2 S65470	pyruvate decarboxy
91	82	4.7	634	2 S56817	probable succinate
92	82	4.7	652	2 S58666	serine/threonine-p
93	82	4.7	658	2 T08153	cysteine proteinas
94	82	4.7	663	2 T25569	hypothetical prote
95	82	4.7	732	2 T01208	starch synthase (E
96	82	4.7	933	2 A31930	cytotactin - chick
97	82	4.7	3011	1 GNWVCH	genome polyprotein
98	81.5	4.7	514	1 ALBSN	alpha-amylase (EC
99	81.5	4.7	535	2 B82358	alkaline serine pr
100	81.5	4.7	795	2 B83755	hypothetical prote
101	81.5	4.7	2477	2 S14428	fibrinectin precur
102	81.5	4.7	3623	2 T09456	intrinsic factor-B

103	81	4.6	378	2	S36506	E2 protein - human	176	78.5	4.5	2481	2	A43908	fibronectin - Afri
104	81	4.6	432	2	A27447	cytotoxic T-lympho	177	78	4.5	349	2	T06207	cysteine proteinas
105	81	4.6	528	2	G02127	fus-like protein -	178	78	4.5	397	2	E86304	F6i1.9 protein - A
106	81	4.6	603	2	T48154	pyruvate decarboxy	179	78	4.5	404	2	B84745	probable RNA-bindi
107	81	4.6	641	1	A41932	organic solvent to	180	78	4.5	584	2	T06163	beta-fructofuranos
108	81	4.6	792	2	B82756	fibrinogen alpha-I	181	78	4.5	611	2	S60040	alpha-amylase (EC
109	81	4.6	817	2	S77106	hypothetical prote	182	78	4.5	706	2	T12748	NADH2 dehydrogenas
110	81	4.6	872	2	H75564	probable ATP-depen	183	78	4.5	795	2	T43447	hypothetical prote
111	81	4.6	890	2	T35237	probable secreted	184	78	4.5	813	2	A40601	ferripyoverdine re
112	81	4.6	940	2	AD1374	internalin protein	185	78	4.5	815	2	H83345	ferripyoverdine re
113	81	4.6	1028	2	T03516	probable outer mem	186	78	4.5	986	2	S12021	thermoactive cellu
114	81	4.6	2403	2	A59386	sanko - human	187	78	4.5	1963	2	T49914	callose synthase c
115	80.5	4.6	319	2	T40156	sun family protein	188	77.5	4.4	189	1	CUMOI	insecticyanin - to
116	80.5	4.6	334	2	T20524	hypothetical prote	189	77.5	4.4	206	2	S22401	insecticyanin B -
117	80.5	4.6	375	2	T33797	hypothetical prote	190	77.5	4.4	577	2	T02401	probable beta-gluc
118	80.5	4.6	548	1	HYBSS	bacillolysin (EC 3	191	77.5	4.4	586	2	T52148	transport protein
119	80.5	4.6	841	2	E71808	probable iron (III	192	77.5	4.4	597	2	S76209	probable flavoprot
120	80.5	4.6	867	1	C64785	outer membrane ush	193	77.5	4.4	635	2	D82770	threonyl-trNA synt
121	80.5	4.6	869	2	E85553	hypothetical prote	194	77.5	4.4	640	2	S34793	succinate dehydrog
122	80.5	4.6	869	2	B90703	probable outer mem	195	77.5	4.4	677	2	JC7202	glucan 1,4-alpha-m
123	80.5	4.6	3566	1	A40701	tenascin-X precurs	196	77.5	4.4	830	2	S15720	glutenin high mole
124	80.5	4.6	4199	2	S76412	hypothetical prote	197	77.5	4.4	842	2	H64694	iron(III) dicitrat
125	80	4.6	297	2	D69866	pyruvate decarboxy	198	77.5	4.4	1234	1	NBMSH	complement factor
126	80	4.6	405	2	S65471	hypothetical prote	199	77.5	4.4	1258	2	JQ0188	ice nucleation pro
127	80	4.6	432	2	I56934	fibrinogen-like pr	200	77.5	4.4	1268	2	B36502	insulin receptor-r
128	80	4.6	439	2	I37391	fibrinogen-like pr	201	77.5	4.4	3016	2	S77300	hypothetical prote
129	80	4.6	815	2	B30843	glutenin high mole	202	77	4.4	240	1	JS0591	endo-1,4-beta-xyla
130	80	4.6	946	2	G71617	SERA antigen/papai	203	77	4.4	274	2	T31528	hypothetical prote
131	80	4.6	1519	2	S41525	major ring-forming	204	77	4.4	286	2	D83762	transcription regu
132	80	4.6	1746	1	A47172	tenascin precursor	205	77	4.4	390	2	E84066	hypothetical prote
133	79.5	4.6	323	2	A47172	transforming growt	206	77	4.4	392	2	T25213	hypothetical prote
134	79.5	4.6	372	2	A42778	agglutinin precurs	207	77	4.4	418	2	AF2045	sugar transport sy
135	79.5	4.6	385	2	T26404	hypothetical prote	208	77	4.4	437	1	FGHUG	fibrinogen gamma-A
136	79.5	4.6	626	2	T01485	probable polygalac	209	77	4.4	453	1	FGHUGB	fibrinogen gamma-B
137	79.5	4.6	750	2	T10864	transcription acti	210	77	4.4	459	2	A25928	cellulase (EC 3.2.
138	79.5	4.6	796	2	E87636	TonB-dependent rec	211	77	4.4	460	2	JC1299	endo-beta-1,4-gluc
139	79.5	4.6	970	2	I78842	receptor protein-t	212	77	4.4	461	2	T20163	hypothetical prote
140	79.5	4.6	986	2	T03760	pullulanase (EC 3.	213	77	4.4	464	2	JC7143	endoglucanase I -
141	79.5	4.6	1196	2	A29130	beta-amylase (EC 3	214	77	4.4	551	2	B64005	hypothetical prote
142	79.5	4.6	1236	1	QZFF	rudimentary protei	215	77	4.4	564	1	HMIVF5	hemagglutinin prec
143	79.5	4.6	2489	2	I73012	complement C3b/C4b	216	77	4.4	614	2	AB0935	vitamin B12 recept
144	79.5	4.6	2761	2	FGRTGA	hypothetical prote	217	77	4.4	618	2	A35827	thrombin (EC 3.4.2
145	79	4.5	437	1	FGRTGB	fibrinogen gamma-A	218	77	4.4	668	2	A46013	coagulation factor
146	79	4.5	445	1	FGRTGB	fibrinogen gamma-B	219	77	4.4	757	2	AI3179	agrobacterium viru
147	79	4.5	448	2	C98122	choline binding pr	220	77	4.4	860	2	I48839	tenascin-X - mouse
148	79	4.5	544	2	S76859	hypothetical prote	221	77	4.4	866	1	C64834	probable outer mem
149	79	4.5	649	2	AH3546	outer membrane pro	222	77	4.4	1358	2	S64356	phosphoribosylform
150	79	4.5	919	2	S33942	hexon protein - hu	223	77	4.4	4006	2	T09070	probable tenascin
151	79	4.5	928	2	T20035	hypothetical prote	224	76.5	4.4	154	2	B69840	conserved hypothet
152	79	4.5	971	2	H71719	hypothetical prote	225	76.5	4.4	241	2	T37005	endo-1,4-beta-xyla
153	78.5	4.5	300	2	E71534	probable pbp2b met	226	76.5	4.4	453	2	A41640	vestigial protein
154	78.5	4.5	302	2	D81692	conserved hypothet	227	76.5	4.4	464	1	B59200	acid phosphatase (
155	78.5	4.5	412	2	C84518	hypothetical prote	228	76.5	4.4	479	2	B87301	aldehyde dehydroge
156	78.5	4.5	482	2	B31795	collagen alpha 1(X	229	76.5	4.4	533	2	C97324	beta-xylosidase, f
157	78.5	4.5	535	2	T32139	hypothetical prote	230	76.5	4.4	541	2	D83684	hypothetical prote
158	78.5	4.5	698	2	T01209	starch synthase (E	231	76.5	4.4	699	2	A38368	chitinase (EC 3.2.
159	78.5	4.5	698	2	F64839	yegH protein precu	232	76.5	4.4	706	2	AD0173	conserved hypothet
160	78.5	4.5	764	2	H83055	probable outer mem	233	76.5	4.4	716	2	JQ1366	polyprotein - hepa
161	78.5	4.5	770	2	S76095	hypothetical prote	234	76.5	4.4	763	2	I50807	complement factor
162	78.5	4.5	781	2	T35029	hypothetical prote	235	76.5	4.4	941	2	T32449	hypothetical prote
163	78.5	4.5	837	2	H87638	TonB-dependent rec	236	76.5	4.4	1322	2	S07053	ice nucleation pro
164	78.5	4.5	900	2	T19689	hypothetical prote	237	76.5	4.4	1456	1	A36563	mannose receptor p
165	78.5	4.5	914	2	C69284	surface layer prot	238	76.5	4.4	2229	2	T16199	hypothetical prote
166	78.5	4.5	1002	2	C86026	probable oxidoredu	239	76	4.4	337	2	A81101	C-5 cytosine-speci
167	78.5	4.5	1002	2	C71513	probable oxidoredu	240	76	4.4	433	1	S22284	transcription regu
168	78.5	4.5	1005	2	C71513	hypothetical prote	241	76	4.4	448	2	C95257	choline binding pr
169	78.5	4.5	1139	1	E64234	cytadherence-acces	242	76	4.4	452	2	T26827	hypothetical prote
170	78.5	4.5	1249	2	S68431	tripeptidyl-peptid	243	76	4.4	460	2	I40799	endo-1,4-beta-gluc
171	78.5	4.5	1262	2	I48855	tripeptidyl-peptid	244	76	4.4	475	2	S48132	metalloprotease
172	78.5	4.5	1431	2	A45866	dextranucrase (EC	245	76	4.4	515	1	NI2JAM	nitrogenase (EC 1.
173	78.5	4.5	1436	2	A46496	antigen WC1.1 prec	246	76	4.4	564	1	HMIVF2	hemagglutinin prec
174	78.5	4.5	1838	1	CGHU1V	collagen alpha 1(V	247	76	4.4	565	2	T16318	hypothetical prote
175	78.5	4.5	2014	2	I36936	complement recepto	248	76	4.4	583	2	S34785	catechol oxidase (

249 76 4.4 592 2 T48155 pyruvate decarboxy  
250 76 4.4 642 1 S34416 transcription fact  
251 76 4.4 660 2 S70904 transferrin-bindin  
252 76 4.4 747 2 H82943 hypothetical prote  
253 76 4.4 828 2 S52393 beta-galactosidase  
254 76 4.4 872 2 S49538 CooC protein precu  
255 76 4.4 1608 2 A28182 hemolysin A - Serr  
256 75.5 4.3 324 2 S20981 chitinase (EC 3.2.  
257 75.5 4.3 445 2 T44482 lysine 6-monooxyge  
258 75.5 4.3 473 2 A48949 beta-glucosidase,  
259 75.5 4.3 484 2 E84765 hypothetical prote  
260 75.5 4.3 510 2 D70480 acetyl-coenzyme A  
261 75.5 4.3 536 2 A34901 lysine carboxypept  
262 75.5 4.3 641 2 AI2524 hypothetical prote  
263 75.5 4.3 657 2 E81119 tail fibre protein  
264 75.5 4.3 703 2 T13074 NADH2 dehydrogenas  
265 75.5 4.3 705 1 C1HURB complement subcomp  
266 75.5 4.3 708 2 AH2626 ferrichrome iron r  
267 75.5 4.3 736 2 T19366 hypothetical prote  
268 75.5 4.3 747 2 G97408 fegA protein U6140  
269 75.5 4.3 784 2 AI0513 organic solvent to  
270 75.5 4.3 867 2 D82940 conserved hypothet  
271 75.5 4.3 881 2 T31818 hypothetical prote  
272 75.5 4.3 1026 1 TLBP74 tail fiber protein  
273 75.5 4.3 1647 2 T32934 hypothetical prote  
274 75.5 4.3 2338 2 T25810 MIBPI protein - ra  
275 75.5 4.3 2437 2 S53611 genome polyprotein  
276 75.5 4.3 3411 1 GNWVY genome polyprotein  
277 75.5 4.3 3411 1 GNWVYP hypothetical prote  
278 75 4.3 238 2 T52505 1-phosphatidylinos  
279 75 4.3 324 2 AB0767 probable CDP-6-deo  
280 75 4.3 329 2 A33493 pectate lyase pelB  
281 75 4.3 330 1 S15303 probable DNA ligas  
282 75 4.3 345 2 E69674 oxidoreductase, Gf  
283 75 4.3 358 2 D70797 probable membrane  
284 75 4.3 376 2 D87451 hypothetical prote  
285 75 4.3 475 2 S49886 hypothetical prote  
286 75 4.3 551 2 T16557 lamin B1 - human  
287 75 4.3 584 2 T18908 lamin B - mouse  
288 75 4.3 586 1 VEHULB probable ATP-depen  
289 75 4.3 587 2 S07720 gene pointed prote  
290 75 4.3 617 2 S62003 transferrin-bindin  
291 75 4.3 623 1 S33167 hypothetical prote  
292 75 4.3 711 2 S70660 alpha-amylase (EC  
293 75 4.3 714 2 T00942 gene pointed prote  
294 75 4.3 717 1 S28784 classical-compleme  
295 75 4.3 718 1 S33168 conserved hypothet  
296 75 4.3 760 1 C2MS probable arabinosy  
297 75 4.3 818 2 F87327 WD-repeat protein  
298 75 4.3 1083 2 H86921 structural polypro  
299 75 4.3 1191 2 AF2501 genome polyprotein  
300 75 4.3 1240 1 VHWVEV structural polypro  
301 75 4.3 1241 2 S26373 structural polypro  
302 75 4.3 1242 2 A56605 structural polypro  
303 75 4.3 1242 2 S72350 tail fiber protein  
304 75 4.3 1341 2 S09579 hypothetical prote  
305 75 4.3 1404 2 E85509 ficolin-beta - pig  
306 74.5 4.3 326 2 B47172 probable membrane  
307 74.5 4.3 330 2 T34972 metalloendopeptida  
308 74.5 4.3 334 2 JE0231 membrane protein,  
309 74.5 4.3 335 2 T03230 protein F59B1.6 [i  
310 74.5 4.3 359 2 D89007 probable membrane  
311 74.5 4.3 367 2 B97317 hypothetical prote  
312 74.5 4.3 455 2 F96817 hypothetical prote  
313 74.5 4.3 478 2 T21144 alpha-amylase (EC  
314 74.5 4.3 512 1 ALBSL hypothetical prote  
315 74.5 4.3 560 2 T16833 genome polyprotein  
316 74.5 4.3 640 2 JQ1584 F25A4.24 [imported  
317 74.5 4.3 642 2 C96777 metalloproteinase  
318 74.5 4.3 922 2 T37256 protein-tyrosine k  
319 74.5 4.3 984 2 A39753 pilY1 protein - ps  
320 74.5 4.3 1161 2 S72645 kinase anchor prot  
321 74.5 4.3 1280 2 T42514

322 74.5 4.3 1353 1 JH0675 restrictin precurs  
323 74.5 4.3 2425 2 D69426 surface layer prot  
324 74.5 4.3 2871 2 A55624 fibrillin-1 precur  
325 74 4.2 187 2 S20044 opacity protein op  
326 74 4.2 240 1 S47512 endo-1,4-beta-xyla  
327 74 4.2 241 2 S71473 endo-1,4-beta-xyla  
328 74 4.2 280 2 AC1502 hypothetical prote  
329 74 4.2 316 2 F89791 peptidoglycan hydr  
330 74 4.2 341 2 T07145 epoxide hydrolase  
331 74 4.2 350 2 B43670 sulfate-binding pr  
332 74 4.2 365 2 A26459 helix-destabilizin  
333 74 4.2 380 2 E88421 protein R74.2 [imp  
334 74 4.2 437 2 JC7138 alpha-amylase (EC  
335 74 4.2 437 2 JT0946 alpha-amylase 3E -  
336 74 4.2 455 2 E96817 hypothetical prote  
337 74 4.2 489 2 C70707 probable aldehyde  
338 74 4.2 503 2 C97262 N-terminal domain  
339 74 4.2 536 2 T51771 poly(3-hydroxybuty  
340 74 4.2 548 2 AF1231 alpha,alpha-phosph  
341 74 4.2 549 2 T20720 hypothetical prote  
342 74 4.2 557 2 D97210 extracellular neut  
343 74 4.2 589 2 T23881 hypothetical prote  
344 74 4.2 596 1 S33540 catechol oxidase (  
345 74 4.2 596 2 AI1865 hypothetical prote  
346 74 4.2 616 1 A40457 replication protei  
347 74 4.2 669 2 T05212 hypothetical prote  
348 74 4.2 827 2 AC2963 celB protein [impo  
349 74 4.2 829 2 T19494 hypothetical prote  
350 74 4.2 837 2 H84239 dimethylsulfoxide  
351 74 4.2 881 2 B98320 cellulose synthase  
352 74 4.2 975 2 A86258 protein F5011.4 [i  
353 74 4.2 1404 2 E90658 RhsG core protein  
354 74 4.2 1466 2 T17138 CuiAA protein - ra  
355 74 4.2 1467 2 T18411 latrophilin-1, bra  
356 74 4.2 1471 2 T17149 CuiBA protein - ra  
357 74 4.2 1472 2 T18413 latrophilin-1, bra  
358 74 4.2 1503 2 T18266 cycloinulo-oligosa  
359 74 4.2 1510 2 T17145 CuiAB protein - ra  
360 74 4.2 1515 2 T17156 CuiBB protein - ra  
361 74 4.2 3010 1 GNWVTW genome polyprotein  
362 73.5 4.2 325 2 S32768 peroxidase (EC 1.1  
363 73.5 4.2 356 2 T21681 hypothetical prote  
364 73.5 4.2 368 2 S47312 cysteine proteinas  
365 73.5 4.2 483 2 H72640 hypothetical prote  
366 73.5 4.2 512 2 T23035 hypothetical prote  
367 73.5 4.2 574 2 C82301 endoglucanase-rela  
368 73.5 4.2 583 1 JC2545 acid phosphatase (  
369 73.5 4.2 590 2 A41335 microbial metallo  
370 73.5 4.2 618 2 H70552 probable PPE prote  
371 73.5 4.2 774 1 JQ0550 1,4-alpha-glucan b  
372 73.5 4.2 834 2 S66498 M-sema F protein p  
373 73.5 4.2 908 2 JN0819 transferrin-bindin  
374 73.5 4.2 1016 2 T41720 hypothetical prote  
375 73.5 4.2 1018 1 S73720 cytdherence acces  
376 73.5 4.2 1166 1 E65151 hypothetical 126K  
377 73.5 4.2 1322 2 D82685 phosphoribosylform  
378 73.5 4.2 2183 2 T37218 hypothetical prote  
379 73.5 4.2 3011 1 S40770 genome polyprotein  
380 73.5 4.2 4307 2 T20721 hypothetical prote  
381 73 4.2 99 2 F82467 probable plasmid s  
382 73 4.2 165 2 A28351 pancreatic stone p  
383 73 4.2 361 2 AG0169 phosphoserine tran  
384 73 4.2 380 2 JN0594 pectate lyase (EC  
385 73 4.2 423 2 T19581 hypothetical prote  
386 73 4.2 438 2 A32670 fibrinogen gamma c  
387 73 4.2 441 2 JC7653 pectate lyase (EC  
388 73 4.2 480 2 T04021 cellulase (EC 3.2.  
389 73 4.2 484 2 S66713 hypothetical prote  
390 73 4.2 496 2 AI2013 UDP-N-acetylmuramo  
391 73 4.2 503 2 S31940 starch-degrading e  
392 73 4.2 518 2 T05277 dihydrofolate redu  
393 73 4.2 527 2 B70700 hypothetical prote  
394 73 4.2 556 1 S31330 inulinase (EC 3.2.



395	73	4.2	564	1	HMIVF7	hemagglutinin prec	468	72	4.1	1254	1	VHVVVT	structural polypro
396	73	4.2	565	1	HMIVTN	hemagglutinin prec	469	72	4.1	1255	1	B44213	structural polypro
397	73	4.2	617	2	S10511	thrombin (EC 3.4.2	470	72	4.1	1281	2	T15762	hypothetical prote
398	73	4.2	627	2	E95107	choline binding pr	471	72	4.1	1363	2	T43220	insulin-like growt
399	73	4.2	758	2	S30948	ferrichrome recept	472	72	4.1	1487	2	S48719	phospholipase-A(2)
400	73	4.2	762	2	JC7174	N,N-dimethylformam	473	72	4.1	1943	2	B64596	toxin-like outer m
401	73	4.2	939	2	T32521	hypothetical prote	474	72	4.1	2535	2	AC0304	probable hemolysin
402	73	4.2	1180	2	E86719	hypothetical prote	475	71.5	4.1	137	2	S34152	ig mu chain - axol
403	73	4.2	1217	2	S52714	sericin1B - silkwo	476	71.5	4.1	189	2	T37368	probable 21.5K pro
404	73	4.2	1239	1	VHVVVE	structural polypro	477	71.5	4.1	199	2	AC3120	superoxide dismuta
405	73	4.2	2187	2	S60224	polyketide synthas	478	71.5	4.1	234	2	C90837	hypothetical prote
406	72.5	4.1	189	2	B42514	H2R protein - vacc	479	71.5	4.1	240	2	D98167	superoxide dismuta
407	72.5	4.1	206	2	S22400	insecticyanin A -	480	71.5	4.1	345	2	B83737	pectate lyase BH06
408	72.5	4.1	214	2	S44706	opacity protein op	481	71.5	4.1	363	2	B86229	hypothetical prote
409	72.5	4.1	282	2	F82748	hypothetical prote	482	71.5	4.1	372	2	T09617	isoliqurritigenin
410	72.5	4.1	298	2	G65006	hypothetical prote	483	71.5	4.1	379	2	A64144	hypothetical prote
411	72.5	4.1	339	2	G82864	hypothetical prote	484	71.5	4.1	418	1	H69351	probable vtpJ-ther
412	72.5	4.1	445	2	T33617	hypothetical prote	485	71.5	4.1	465	2	T51094	acid phosphatase (
413	72.5	4.1	512	2	T13635	probable minor str	486	71.5	4.1	473	1	A59200	acid phosphatase (
414	72.5	4.1	549	2	JC5926	secreted klotho pr	487	71.5	4.1	482	2	C72254	glycerol kinase -
415	72.5	4.1	562	2	A41707	oligo-1,6-glucosid	488	71.5	4.1	496	2	JE0390	glycerol kinase (E
416	72.5	4.1	587	2	S36231	beta-fructofuranos	489	71.5	4.1	513	2	D88991	protein apx-1 [imp
417	72.5	4.1	590	2	T02096	probable beta-fruc	490	71.5	4.1	516	2	S42093	cellulose 1,4-beta
418	72.5	4.1	617	2	E72803	gp31 protein - Myc	491	71.5	4.1	524	2	T08931	hypothetical prote
419	72.5	4.1	632	2	T02627	hypothetical prote	492	71.5	4.1	575	2	T12094	beta-fructofuranos
420	72.5	4.1	641	2	S41434	gene NS-1 protein	493	71.5	4.1	598	2	S63617	cymH protein - Kle
421	72.5	4.1	662	2	T48128	probable reverse t	494	71.5	4.1	627	2	T32958	hypothetical prote
422	72.5	4.1	702	2	T12624	NADH2 dehydrogenas	495	71.5	4.1	630	2	JQ1670	polygalacturonase
423	72.5	4.1	752	2	S61505	glycogen(starch) s	496	71.5	4.1	631	2	S70908	succinate dehydrog
424	72.5	4.1	787	2	G64620	iron(III) dicitrat	497	71.5	4.1	634	2	T51815	ABC transporter AT
425	72.5	4.1	804	2	T14762	hypothetical prote	498	71.5	4.1	635	2	AG3631	fibrinogen alpha c
426	72.5	4.1	818	2	T02231	probable isoamylas	499	71.5	4.1	644	1	FGHUA	Quinol oxidase pol
427	72.5	4.1	934	2	T25864	hypothetical prote	500	71.5	4.1	662	2	B89875	transcription fact
428	72.5	4.1	1012	2	JC5925	membrane klotho pr	501	71.5	4.1	667	2	A41311	hypothetical prote
429	72.5	4.1	1261	2	T50065	hypothetical prote	502	71.5	4.1	670	2	D86176	probable outer mem
430	72.5	4.1	1396	2	T10627	hypothetical prote	503	71.5	4.1	696	2	G71829	hypothetical prote
431	72.5	4.1	1422	2	T42636	protein-tyrosine-p	504	71.5	4.1	738	2	T00343	hypothetical prote
432	72.5	4.1	1888	2	T14273	zinc finger protei	505	71.5	4.1	751	2	T15403	hypothetical prote
433	72.5	4.1	2180	2	T29764	hypothetical prote	506	71.5	4.1	767	2	F64605	iron(III) dicitrat
434	72.5	4.1	2214	2	T16305	hypothetical prote	507	71.5	4.1	785	1	WMBEK8	infected cell prot
435	72.5	4.1	2480	2	D84904	hypothetical prote	508	71.5	4.1	785	1	WMBEW8	infected cell prot
436	72.5	4.1	3133	2	S52093	hemocytin - silkwo	509	71.5	4.1	789	2	T01321	probable isoamylas
437	72	4.1	282	2	H97226	protein containing	510	71.5	4.1	833	2	C97901	leucine-tRNA ligas
438	72	4.1	307	1	S53962	hypothetical prote	511	71.5	4.1	839	2	A56337	glycoprotein phosp
439	72	4.1	308	2	T29754	hypothetical prote	512	71.5	4.1	859	2	F55545	outer membrane ush
440	72	4.1	309	2	G75286	serine proteinase	513	71.5	4.1	1029	2	F87369	TonB-dependent rec
441	72	4.1	329	2	S08627	chitinase (EC 3.2.	514	71.5	4.1	1090	2	JC1421	leucine-tRNA ligas
442	72	4.1	357	2	A95888	probable ABC trans	515	71.5	4.1	1229	2	F90040	respiratory nitrat
443	72	4.1	400	2	T24258	hypothetical prote	516	71.5	4.1	1255	1	D44213	structural polypro
444	72	4.1	402	1	JU0332	alkaline proteinas	517	71.5	4.1	1315	2	T28679	fibrinogen-binding
445	72	4.1	479	2	T40683	cell cycle protein	518	71.5	4.1	1742	2	T17120	cellulase (EC 3.2.
446	72	4.1	491	2	T06798	probable starch sy	519	71.5	4.1	1999	2	AB2018	hypothetical prote
447	72	4.1	496	2	T23565	hypothetical prote	520	71.5	4.1	2178	2	S55805	alpha-toxin - C1os
448	72	4.1	504	2	S12164	serralysin (EC 3.4	521	71.5	4.1	2524	2	A35844	Xotch protein - Af
449	72	4.1	507	2	S56143	cell cycle protein	522	71.5	4.1	2629	2	T32735	telomerase-associa
450	72	4.1	550	2	S65753	beta-fructofuranos	523	71.5	4.1	3011	1	GNWVC3	genome polyprote
451	72	4.1	564	1	HMIVF8	hemagglutinin prec	524	71.5	4.1	3300	2	D70575	probable PPE prote
452	72	4.1	564	1	HMIVF1	hemagglutinin prec	525	71	4.1	166	2	E96607	hypothetical prote
453	72	4.1	583	2	S01496	lamin B - African	526	71	4.1	198	2	T06813	dehydrin 3 - garde
454	72	4.1	603	2	T22111	hypothetical prote	527	71	4.1	280	2	T02004	chitinase (EC 3.2.
455	72	4.1	627	2	G97975	hypothetical prote	528	71	4.1	322	2	T07924	probable starch sy
456	72	4.1	722	2	T30995	hypothetical prote	529	71	4.1	326	2	E84812	hypothetical prote
457	72	4.1	767	2	T30018	hypothetical prote	530	71	4.1	336	2	AH1212	hypothetical prote
458	72	4.1	780	1	WMBEH8	infected cell prot	531	71	4.1	348	2	A43358	TN916 ORF14 and to
459	72	4.1	815	2	JN0689	glutenin, high-mol	532	71	4.1	373	1	AJHYQ	macrophage capping
460	72	4.1	821	2	E87503	1,4-beta-D-glucan	533	71	4.1	373	1	AJHYQ	glutamate-ammonia
461	72	4.1	836	1	S25218	outer membrane ush	534	71	4.1	445	2	E86493	Pmp_5 [imported] -
462	72	4.1	937	2	A56517	nucleoporin Nup98	535	71	4.1	468	2	T49117	glucosidase like p
463	72	4.1	952	2	F96498	protein-tyrosine k	536	71	4.1	486	1	HYSE15	serralysin (EC 3.4
464	72	4.1	953	2	I50612	hypothetical prote	537	71	4.1	488	2	T42038	catalase (EC 1.11.
465	72	4.1	1144	2	A36968	p1-like adhesin pr	538	71	4.1	506	2	S37276	hexon protein - hu
466	72	4.1	1250	2	T27706	hypothetical prote	539	71	4.1	508	1	VGVNFR	spike glycoprotein
467	72	4.1	1254	1	VHVVVE	structural polypro	540	71	4.1	509	2	E90071	zinc metalloprotei
										533	2	B56110	tyrosine phosphopr

541	71	4.1	561	2	G96752	unknown protein F2	614	70	4.0	295	2	A64756	attaching and effa
542	71	4.1	570	2	A45249	alpha-glucosidase	615	70	4.0	389	1	S39720	probable hydro-ly
543	71	4.1	570	2	T32743	hypothetical prote	616	70	4.0	419	2	JC4522	alpha-galactosidas
544	71	4.1	574	2	T16230	hypothetical prote	617	70	4.0	430	2	S69913	hypertension-assoc
545	71	4.1	588	2	T26193	hypothetical prote	618	70	4.0	434	2	T32520	hypothetical prote
546	71	4.1	603	2	T03295	pyruvate decarboxy	619	70	4.0	462	4	S33798	FUS/CHOP mutant fu
547	71	4.1	627	2	B83692	hypothetical prote	620	70	4.0	468	2	T49682	hypothetical prote
548	71	4.1	654	2	AG0995	glycogen operon pr	621	70	4.0	471	2	C71439	hypothetical prote
549	71	4.1	657	2	E81901	probable phage tai	622	70	4.0	479	2	T05588	cellulase (EC 3.2.
550	71	4.1	681	2	E82812	outer membrane hem	623	70	4.0	483	2	D71439	probable Beta-Amyl
551	71	4.1	686	1	A59271	Ra-reactive factor	624	70	4.0	514	2	B64634	hypothetical prote
552	71	4.1	787	2	C84898	hypothetical prote	625	70	4.0	523	2	F86481	S9.2K hypothetical
553	71	4.1	792	2	F71894	iron (III) dicitra	626	70	4.0	526	1	S33799	RNA-binding protei
554	71	4.1	833	1	A31593	heat shock transcr	627	70	4.0	527	2	E86432	T5I8.15 protein -
555	71	4.1	888	2	S28791	collagen alpha 1(X	628	70	4.0	531	2	T04722	hypothetical prote
556	71	4.1	906	2	G90281	conserved hypothet	629	70	4.0	548	2	B87596	xylosidase/arabino
557	71	4.1	919	2	T16693	hypothetical prote	630	70	4.0	552	2	JC7666	serine-type carbox
558	71	4.1	957	2	A84089	hypothetical prote	631	70	4.0	553	2	C84920	hypothetical prote
559	71	4.1	1060	2	T31763	hypothetical prote	632	70	4.0	564	1	HM1VF4	hemagglutinin prec
560	71	4.1	1230	2	T17187	CL3AB protein - ra	633	70	4.0	566	1	HYBSU	bacillolysin (EC 3
561	71	4.1	1273	2	T17188	CL3AC protein - ra	634	70	4.0	575	1	S03745	beta-amylase (EC 3
562	71	4.1	1274	2	T10729	transferrin-like p	635	70	4.0	583	2	S30930	catechol oxidase (
563	71	4.1	1298	2	T17199	CL3BB protein - ra	636	70	4.0	585	2	C49596	genome polypotein
564	71	4.1	1341	2	T17200	CL3BC protein - ra	637	70	4.0	591	2	S33542	catechol oxidase (
565	71	4.1	1459	2	T17186	CL3AA protein - ra	638	70	4.0	600	2	B86854	hypothetical prote
566	71	4.1	1508	2	T31098	probable dextranu	639	70	4.0	638	2	B83890	hypothetical prote
567	71	4.1	1518	2	D96660	protein F2K11.14 [	640	70	4.0	686	2	S28042	hemin receptor pre
568	71	4.1	1527	2	T17198	CL3BA protein - ra	641	70	4.0	701	2	T13587	NADH2 dehydrogenas
569	71	4.1	1548	2	S34583	serine proteinase	642	70	4.0	738	2	S14270	alcohol dehydrogen
570	71	4.1	1550	2	T14327	alpha-latrotoxin r	643	70	4.0	738	2	T00748	4-alpha-glucanotra
571	71	4.1	1705	2	F71414	hypothetical prote	644	70	4.0	757	2	C70034	conserved hypothet
572	71	4.1	3010	1	A45573	genome polypotein	645	70	4.0	761	2	AI0074	probable autotrans
573	70.5	4.0	248	2	T04758	hypothetical prote	646	70	4.0	819	2	AI3197	TonB-dependent rec
574	70.5	4.0	285	2	D90010	hypothetical prote	647	70	4.0	822	2	AB0238	heamin storage sys
575	70.5	4.0	314	2	JH0389	conserved hypothet	648	70	4.0	822	2	T47007	hypothetical prote
576	70.5	4.0	365	1	MMBPP2	pectin lyase (EC 4	649	70	4.0	879	2	F85875	probable fimbrial
577	70.5	4.0	373	1	AJRTQ	outer membrane por	650	70	4.0	879	2	E91031	probable outer mem
578	70.5	4.0	399	1	S35719	glutamate-ammonia	651	70	4.0	949	2	T08658	hypothetical prote
579	70.5	4.0	484	2	JU0091	transcription fact	652	70	4.0	1291	2	T13389	hypothetical prote
580	70.5	4.0	510	2	AF1182	sucrose alpha-gluc	653	70	4.0	1417	2	H90670	probable adhesin [
581	70.5	4.0	525	1	KGHUGH	oligo-1,6-glucosid	654	70	4.0	1417	2	D85521	probable adhesin e
582	70.5	4.0	559	2	H83758	histidine-rich gly	655	70	4.0	1545	2	B41859	IgA-specific metal
583	70.5	4.0	566	2	S69887	alpha,alpha-phoepp	656	70	4.0	1569	2	A65044	hypothetical prote
584	70.5	4.0	594	2	E96667	hemagglutinin prec	657	70	4.0	2233	2	T28669	surface protein 51
585	70.5	4.0	594	2	T15291	unknown protein, 6	658	70	4.0	3010	1	GNWVTC	genome polypotein
586	70.5	4.0	605	2	S57821	sphingomyelin phos	659	69.5	4.0	168	2	PN0680	nitrogenase (EC 1.
587	70.5	4.0	639	2	JQ0607	pyruvate decarboxy	660	69.5	4.0	189	1	QQVZH2	H2 protein - vacci
588	70.5	4.0	642	1	S52111	glucan 1,4-alpha-g	661	69.5	4.0	276	2	T09131	chitinase (EC 3.2.
589	70.5	4.0	649	2	T32668	uromodulin precurs	662	69.5	4.0	314	2	C64045	2-dehydro-3-deoxyg
590	70.5	4.0	653	2	F85620	hypothetical prote	663	69.5	4.0	323	2	JC5691	cysteine proteinas
591	70.5	4.0	653	2	H90756	partial fimbrial u	664	69.5	4.0	373	1	AJHUQ	glutamate-ammonia
592	70.5	4.0	686	2	A55665	partial fimbrial u	665	69.5	4.0	374	2	AH0149	outer membrane pro
593	70.5	4.0	695	2	T13639	microtubule-associ	666	69.5	4.0	390	2	T39818	hypothetical prote
594	70.5	4.0	712	2	F97012	probable tail-host	667	69.5	4.0	401	2	S65138	glycoprotein antig
595	70.5	4.0	746	2	A97979	hypothetical prote	668	69.5	4.0	427	2	S74211	PAS-6/7 protein pr
596	70.5	4.0	793	2	H82594	competence protein	669	69.5	4.0	448	2	JW0037	beta-glucosidase (
597	70.5	4.0	812	2	AG3138	ferric enterobacti	670	69.5	4.0	449	1	NBHUHS	complement factor
598	70.5	4.0	817	2	D87390	fimbrial usher pro	671	69.5	4.0	453	2	D69828	conserved hypothet
599	70.5	4.0	833	2	H95029	hypothetical prote	672	69.5	4.0	454	2	T43069	probable serine pr
600	70.5	4.0	915	2	T21773	TonB-dependent rec	673	69.5	4.0	455	2	G71896	probable outer mem
601	70.5	4.0	927	2	T21772	leucyl-tRNA synthe	674	69.5	4.0	477	2	JS0597	t-plasminogen acti
602	70.5	4.0	944	2	C81798	hypothetical prote	675	69.5	4.0	497	2	G86299	F3O9.24 protein -
603	70.5	4.0	995	2	A56599	hypothetical prote	676	69.5	4.0	528	2	S38242	hypothetical prote
604	70.5	4.0	1034	2	JC2143	lactoferrin bindin	677	69.5	4.0	545	1	B39827	4-coumarate-COA li
605	70.5	4.0	997	2	S73556	embryo kinase 5 -	678	69.5	4.0	555	1	S17502	inulinase (EC 3.2.
606	70.5	4.0	1034	2	D82428	MG414 homolog Cl2	679	69.5	4.0	585	2	T19814	hypothetical prote
607	70.5	4.0	1051	2	H82428	ice nucleation act	680	69.5	4.0	595	2	AG3194	alpha-amylase Atu5
608	70.5	4.0	1138	2	H86201	chitodextrinase VC	681	69.5	4.0	598	2	B75626	PTS system, fructo
609	70.5	4.0	1260	2	H89984	hypothetical prote	682	69.5	4.0	602	2	S71557	pyruvate decarboxy
610	70.5	4.0	1528	2	D85912	hypothetical prote	683	69.5	4.0	611	1	S06047	endo-1,4-beta-xyla
611	70.5	4.0	1571	2	C91068	hypothetical prote	684	69.5	4.0	642	2	B72428	laminarinase - The
612	70.5	4.0	1711	2	T31337	1,4-beta-glucanase	685	69.5	4.0	673	2	AF0232	pesticin/yersiniab
613	70	4.0	271	2	S72382	hypothetical prote	686	69.5	4.0	673	2	A56148	pesticin receptor

687	69.5	4.0	702	1	A48562	coat protein - San	760	69	3.9	3890	2	C89921	hypothetical prote
688	69.5	4.0	720	2	AH0117	ornithine decarbox	761	68.5	3.9	183	2	AI3566	hypothetical prote
689	69.5	4.0	728	2	AF0995	1,4-alpha-glucan b	762	68.5	3.9	206	2	T12743	hypothetical prote
690	69.5	4.0	738	2	A87516	dipeptidyl peptida	763	68.5	3.9	219	2	T21736	hypothetical prote
691	69.5	4.0	746	2	C95110	competence protein	764	68.5	3.9	231	2	AI0372	hypothetical prote
692	69.5	4.0	776	2	S45495	isp4 protein - fis	765	68.5	3.9	245	2	E86450	F5D14.29 protein -
693	69.5	4.0	797	1	VBEX1	glycoprotein X pre	766	68.5	3.9	256	2	S77522	hypothetical prote
694	69.5	4.0	804	2	H75125	hypothetical prote	767	68.5	3.9	259	2	A29831	heat-labile entero
695	69.5	4.0	840	2	G98169	hypothetical prote	768	68.5	3.9	263	2	S72528	chitinase (EC 3.2.
696	69.5	4.0	840	2	AF3117	hypothetical prote	769	68.5	3.9	275	2	T51651	myb-related transc
697	69.5	4.0	866	2	T45462	membrane glycoprot	770	68.5	3.9	306	2	G84729	hypothetical prote
698	69.5	4.0	1063	2	T00624	endo-1,4-beta-xyla	771	68.5	3.9	310	2	C86475	unknown protein, 4
699	69.5	4.0	1170	2	A40558	thrombospondin 1 p	772	68.5	3.9	323	2	T05694	pathogenesis-relat
700	69.5	4.0	1224	1	ERHUAH	coatmer complex a	773	68.5	3.9	328	2	S47047	DTDP-4-dehydroram
701	69.5	4.0	1231	1	NBHUH	complement factor	774	68.5	3.9	366	1	W2WLR1	E2 protein - rhesu
702	69.5	4.0	1365	2	A41483	glucosyltransferas	775	68.5	3.9	373	2	S41452	glutamate-ammonia
703	69.5	4.0	1475	2	B33135	gtfB protein precu	776	68.5	3.9	386	2	S72435	RNA-binding protei
704	69.5	4.0	1520	1	TVFFA	protein-tyrosine k	777	68.5	3.9	396	1	S15992	flavohe moglobin hm
705	69.5	4.0	1561	2	S61314	IGA-specific metal	778	68.5	3.9	396	2	F85900	dihydropteridine r
706	69.5	4.0	1748	2	S42136	cnjB protein - Tet	779	68.5	3.9	396	2	B91056	dihydropteridine r
707	69.5	4.0	3002	2	A47221	fibrillin 1 precur	780	68.5	3.9	413	2	D86920	probable UDP-galac
708	69	3.9	125	2	PH0957	ig heavy chain V r	781	68.5	3.9	440	2	AB1111	B. subtilis yycH p
709	69	3.9	172	2	S75094	hypothetical prote	782	68.5	3.9	465	1	T51095	acid phosphatase (
710	69	3.9	233	2	S36350	opacity protein op	783	68.5	3.9	467	1	PABYCC	acid phosphatase (
711	69	3.9	246	2	AI1625	hypothetical prote	784	68.5	3.9	468	2	F84686	hypothetical prote
712	69	3.9	253	2	JC5014	2,4-dichlorophenol	785	68.5	3.9	486	2	I40548	bifunctional cellu
713	69	3.9	275	2	T03032	chitinase (EC 3.2.	786	68.5	3.9	513	2	S63701	mannosyl-oligosacc
714	69	3.9	288	2	T14863	porin Mip1 - Norwa	787	68.5	3.9	534	2	A29776	glucan 1,4-alpha-g
715	69	3.9	305	2	S73645	probable lipoprote	788	68.5	3.9	546	2	JC4113	neutral proteinase
716	69	3.9	307	2	T38206	probable phosphopr	789	68.5	3.9	546	2	S72176	thermolysin (EC 3.
717	69	3.9	311	2	E96714	probable DNA-bindi	790	68.5	3.9	597	2	T07096	catechol oxidase (
718	69	3.9	380	2	A53809	mitochondrial resp	791	68.5	3.9	609	2	S57378	hypothetical prote
719	69	3.9	397	2	A97197	transglutaminase-1	792	68.5	3.9	611	2	G83177	probable sodium/hy
720	69	3.9	398	2	JQ0366	phospholipase C (E	793	68.5	3.9	619	2	T15969	hypothetical prote
721	69	3.9	399	1	D69056	conserved hypothet	794	68.5	3.9	640	1	ALASGR	glucan 1,4-alpha-g
722	69	3.9	402	2	T02378	hypothetical prote	795	68.5	3.9	640	2	A29166	glucan 1,4-alpha-g
723	69	3.9	416	2	F72640	hypothetical prote	796	68.5	3.9	641	2	S41439	gene NS-1 protein
724	69	3.9	418	2	H95407	probable aminometh	797	68.5	3.9	645	2	G90819	hypothetical prote
725	69	3.9	419	1	S25835	subtilisin (EC 3.4	798	68.5	3.9	661	1	S59633	endo-1,4-beta-xyla
726	69	3.9	431	2	T29850	hypothetical prote	799	68.5	3.9	673	2	S60142	outer membrane pro
727	69	3.9	432	2	AI2613	hypothetical prote	800	68.5	3.9	687	2	S43587	F26F3.2 protein (c
728	69	3.9	432	2	G97395	hypothetical prote	801	68.5	3.9	690	2	F98114	choline-binding pr
729	69	3.9	432	2	D87649	tolB protein [impo	802	68.5	3.9	698	2	A69222	NADH2 dehydrogenas
730	69	3.9	443	2	E65008	hypothetical prote	803	68.5	3.9	698	2	G83443	hypothetical prote
731	69	3.9	444	2	D26421	shufflon B' - Esch	804	68.5	3.9	702	2	B83237	hypothetical prote
732	69	3.9	453	2	S49168	beta tubulin 1 - r	805	68.5	3.9	721	2	T25415	probable TonB-depe
733	69	3.9	455	2	B64860	ymfN protein - Esc	806	68.5	3.9	742	2	T25415	hypothetical prote
734	69	3.9	461	1	KFHU	coagulation factor	807	68.5	3.9	802	2	B81794	probably secreted
735	69	3.9	522	2	T18504	hypothetical prote	808	68.5	3.9	839	2	D97013	probably secreted
736	69	3.9	547	2	S49814	hypothetical prote	809	68.5	3.9	853	2	T07036	lipoxigenase (EC 1
737	69	3.9	579	2	A56740	transferrin-bindin	810	68.5	3.9	926	2	D86897	hypothetical prote
738	69	3.9	617	2	H90551	sperm-egg recognit	811	68.5	3.9	938	2	AF1772	internalin-like pr
739	69	3.9	645	2	G01205	lipoprotein [impor	812	68.5	3.9	985	2	D82776	pyruvate dehydroge
740	69	3.9	655	1	A46688	TYL protein - huma	813	68.5	3.9	1050	2	JC7889	heparinase (EC 3.2
741	69	3.9	682	2	F81332	hepatocyte growth	814	68.5	3.9	1057	2	T15720	hypothetical prote
742	69	3.9	699	2	A54767	probable periplasm	815	68.5	3.9	1210	2	A25547	ice nucleation pro
743	69	3.9	769	2	H97033	transcription fact	816	68.5	3.9	1453	2	S41453	spike protein - ca
744	69	3.9	784	2	E82731	alpha-glucosidase	817	68.5	3.9	1455	1	A48925	mannose receptor p
745	69	3.9	803	2	F83360	outer membrane ant	818	68.5	3.9	1529	2	S69688	hypothetical prote
746	69	3.9	889	2	B55123	glucose dehydrogen	819	68.5	3.9	1684	2	T02367	hypothetical prote
747	69	3.9	890	2	A30481	coatmer complex b	820	68.5	3.9	1876	2	S50235	1,3-beta-glucan sy
748	69	3.9	961	2	AD0548	bacteriocin BCN5 -	821	68.5	3.9	2871	2	A55567	fibrillin I - bovi
749	69	3.9	1021	2	I40805	puative autotransp	822	68.5	3.9	3461	2	S58870	reelin precursor -
750	69	3.9	1098	2	T28816	collagenase - Clos	823	68.5	3.9	5376	2	T42215	zonadhesin - mouse
751	69	3.9	1207	2	T23754	hypothetical prote	824	68	3.9	178	2	E64648	hypothetical prote
752	69	3.9	1335	2	T30211	hypothetical prote	825	68	3.9	256	2	C81348	probable periplasm
753	69	3.9	1390	2	T30346	autolysin E - Stap	826	68	3.9	293	2	AC2780	tolB protein limpo
754	69	3.9	1558	2	C89114	insulin receptor -	827	68	3.9	293	2	E97559	tolb protein precu
755	69	3.9	1578	2	AD1512	protein C37C3.6a (	828	68	3.9	297	2	T30613	hypothetical prote
756	69	3.9	2167	2	T34395	peptidoglycan bou	829	68	3.9	327	2	A70392	UDP-glucose-4-epim
757	69	3.9	3295	2	AE0074	hypothetical prote	830	68	3.9	340	2	D95045	choline binding pr
758	69	3.9	3432	1	GNWVJS	probable adhesin Y	831	68	3.9	351	2	T26840	hypothetical prote
759	69	3.9	3432	1	GNWVJE	genome polyprotein	832	68	3.9	380	2	T23546	hypothetical prote



833	68	3.9	389	2	E86634	hypothetical prote	906	67.5	3.9	498	2	H85190	probable beta-amyl
834	68	3.9	398	2	B49231	phospholipase C, a	907	67.5	3.9	544	2	A42464	microbial metallo
835	68	3.9	407	2	E88976	protein F54E2.1 [i	908	67.5	3.9	547	2	A32803	glucan 1,4-alpha-m
836	68	3.9	417	1	A39904	gastric intrinsic	909	67.5	3.9	548	2	T52556	beta-amylase (EC 3
837	68	3.9	417	2	AB2359	hypothetical prote	910	67.5	3.9	552	2	S19134	probable alpha-glu
838	68	3.9	425	2	C89753	protein F11C7.3 [i	911	67.5	3.9	552	2	AH1915	hypothetical prote
839	68	3.9	439	2	G84432	probable C2H2-type	912	67.5	3.9	566	1	HMIV	hemagglutinin prec
840	68	3.9	440	2	T00583	probable indole-3-	913	67.5	3.9	571	2	C75174	glycyl-tRNA synthe
841	68	3.9	453	2	C86727	beta-glucosidase [	914	67.5	3.9	599	2	G83296	hypothetical prote
842	68	3.9	457	2	T23494	phenylalanine 4-mo	915	67.5	3.9	607	2	S69522	probable terminase
843	68	3.9	469	2	S45453	alpha-galactosidas	916	67.5	3.9	616	2	JC7905	fructan 6-fructosy
844	68	3.9	469	1	NMIVW8	exo-alpha-sialidas	917	67.5	3.9	648	1	JQ1150	protein kinase (EC
845	68	3.9	475	2	T16364	hypothetical prote	918	67.5	3.9	676	2	F91185	alpha-amylase [imp
846	68	3.9	491	2	T21421	hypothetical prote	919	67.5	3.9	676	2	D86032	hypothetical prote
847	68	3.9	503	2	B97262	N-terminal domain	920	67.5	3.9	676	2	S41022	chromogranin B pre
848	68	3.9	514	2	E71880	probable outer mem	921	67.5	3.9	677	1	S09078	protein-glutamine
849	68	3.9	529	2	AC2112	hypothetical prote	922	67.5	3.9	680	2	JC5133	protein-glutamine
850	68	3.9	532	1	CPBYI	carboxypeptidase C	923	67.5	3.9	691	2	C64548	NADH2 dehydrogenas
851	68	3.9	564	1	HMIVF3	hemagglutinin prec	924	67.5	3.9	693	2	A45991	ornithine decarbox
852	68	3.9	588	2	S34786	catechol oxidase (	925	67.5	3.9	702	2	T13058	trimethylamine deh
853	68	3.9	591	1	FOMVMM	gag polyprotein -	926	67.5	3.9	720	2	F64079	DNA-binding protei
854	68	3.9	639	2	JT0479	glucan 1,4-alpha-g	927	67.5	3.9	730	1	S24124	M83 protein - huma
855	68	3.9	672	1	S73715	cytadherence acces	928	67.5	3.9	737	2	S28030	VirB4 type IV secr
856	68	3.9	686	2	T06334	1,4-alpha-glucan b	929	67.5	3.9	771	2	JC7388	tail tubular prote
857	68	3.9	713	2	T21201	hypothetical prote	930	67.5	3.9	792	2	D95351	acetyl-CoA decarbo
858	68	3.9	726	2	T31287	hypothetical prote	931	67.5	3.9	794	1	TLBPB7	hypothetical prote
859	68	3.9	752	2	E72616	hypothetical prote	932	67.5	3.9	798	2	F69549	conserved hypothet
860	68	3.9	753	2	D83081	probable outer mem	933	67.5	3.9	798	2	S09867	hexon protein - hu
861	68	3.9	773	2	A83888	hypothetical prote	934	67.5	3.9	867	2	D87320	carboxymethylcellu
862	68	3.9	790	2	T47959	hypothetical prote	935	67.5	3.9	940	2	S37216	protein K07E3.6 [i
863	68	3.9	815	2	T19704	hypothetical prote	936	67.5	3.9	962	2	S03818	fibrinogen alpha c
864	68	3.9	856	2	T00349	Avicelase III - As	937	67.5	3.9	964	2	H89582	hypothetical prote
865	68	3.9	884	2	H83322	hypothetical prote	938	67.5	3.9	966	2	A33626	hypothetical prote
866	68	3.9	943	2	G81070	lactoferrin-bindin	939	67.5	3.9	989	2	C83035	serine proteinase
867	68	3.9	943	2	T35497	hypothetical prote	940	67.5	3.9	1034	2	JC5569	serine proteinase
868	68	3.9	960	2	JE0356	gamma-aminobutyric	941	67.5	3.9	1036	2	JC5568	probable arabinosy
869	68	3.9	1144	2	A54810	TMV resistance pro	942	67.5	3.9	1094	2	E70697	RNA-directed RNA p
870	68	3.9	1300	2	A36502	insulin receptor-r	943	67.5	3.9	1116	2	T30828	hypothetical prote
871	68	3.9	1347	2	T30909	endo-1,4-beta-xyla	944	67.5	3.9	1227	2	T48028	latrophilin-3, spl
872	68	3.9	1377	2	I54632	tsh protein - Esch	945	67.5	3.9	1231	2	T18390	latrophilin-3, spl
873	68	3.9	1395	2	T00068	hypothetical prote	946	67.5	3.9	1240	2	T18393	latrophilin-3, spl
874	68	3.9	1878	2	E86189	hypothetical prote	947	67.5	3.9	1274	2	T18391	latrophilin-3, spl
875	68	3.9	1906	2	AD2443	hypothetical prote	948	67.5	3.9	1283	2	T18394	latrophilin-3, spl
876	68	3.9	2161	2	JH0564	calcium channel al	949	67.5	3.9	1290	2	A57190	ebnerin precursor
877	68	3.9	2181	2	A38198	calcium channel al	950	67.5	3.9	1299	2	T18398	latrophilin-3, spl
878	68	3.9	2203	2	T42742	voltage-dependent	951	67.5	3.9	1308	2	T18408	latrophilin-3, spl
879	68	3.9	2269	1	JQ1750	genome polyprotein	952	67.5	3.9	1329	2	T29074	hypothetical prote
880	68	3.9	2893	2	A64556	toxin-like outer m	953	67.5	3.9	1342	2	T18405	latrophilin-3, spl
881	68	3.9	3010	1	S18030	genome polyprotein	954	67.5	3.9	1351	2	T18409	latrophilin-3, spl
882	67.5	3.9	136	2	PH0960	ig heavy chain V r	955	67.5	3.9	1361	2	T29435	hypothetical prote
883	67.5	3.9	246	2	AG1263	hypothetical prote	956	67.5	3.9	1375	2	T13822	frazzled gene prot
884	67.5	3.9	250	2	T43153	probable aldehyde	957	67.5	3.9	1444	2	T18856	angiogenesis inhib
885	67.5	3.9	281	2	F86355	T16B15.10 protein	958	67.5	3.9	1503	2	T18389	latrophilin-3, spl
886	67.5	3.9	313	2	T02534	hypothetical prote	959	67.5	3.9	1512	2	T18392	latrophilin-3, spl
887	67.5	3.9	314	2	AD0220	flagellar protein	960	67.5	3.9	1526	2	T13823	frazzled gene prot
888	67.5	3.9	316	2	G86333	hypothetical prote	961	67.5	3.9	1530	2	AH1396	peptidoglycan anch
889	67.5	3.9	350	2	A82299	outer membrane pro	962	67.5	3.9	1537	2	JC4172	DNA (cytosine-5)-
890	67.5	3.9	360	2	T35783	probable secreted	963	67.5	3.9	1571	2	T18395	latrophilin-3, spl
891	67.5	3.9	369	2	S70847	outer membrane por	964	67.5	3.9	1580	2	T18407	latrophilin-3, spl
892	67.5	3.9	372	2	B70661	hypothetical prote	965	67.5	3.9	1844	2	T51890	related to Nup98-N
893	67.5	3.9	377	2	T00152	hypothetical prote	966	67.5	3.9	2013	2	AD1129	probable peptidogl
894	67.5	3.9	386	2	S48755	major surface prot	967	67.5	3.9	2334	2	S32920	cell wall-associat
895	67.5	3.9	390	2	H86253	hypothetical prote	968	67.5	3.9	4976	2	T14165	peptide synthetase
896	67.5	3.9	392	2	I51422	glutamine syntheta	969	67.5	3.9	133	2	A47267	botrocetin alpha c
897	67.5	3.9	420	2	D95972	probable sugar upt	970	67	3.8	197	1	A44597	endo-1,4-beta-xyla
898	67.5	3.9	428	2	G89982	hypothetical prote	971	67	3.8	204	2	T28985	hypothetical prote
899	67.5	3.9	449	2	S16748	proline-rich prote	972	67	3.8	264	2	T40927	hypothetical wfl1
900	67.5	3.9	458	2	T36442	probable serine pr	973	67	3.8	273	2	E81330	probable periplasm
901	67.5	3.9	460	2	JN0663	alpha-amylase (EC	974	67	3.8	288	2	T22721	hypothetical prote
902	67.5	3.9	467	1	LIDG	triacylglycerol li	975	67	3.8	319	2	T32435	hypothetical prote
903	67.5	3.9	484	2	H95200	sucrose-6-phosphat	976	67	3.8	340	2	C71266	conserved hypothet
904	67.5	3.9	484	2	F98067	beta-fructofuranos	977	67	3.8	361	1	XNEBPY	phosphoserine tran
905	67.5	3.9	494	2	A89985	hypothetical prote	978	67	3.8	364	2	T25124	hypothetical prote

979	67	3.8	366	2	B69949	phage-related prot	1052	66.5	3.8	418	2	F95245	tyrosyl-tRNA synth
980	67	3.8	375	2	A46174	RNA-binding protei	1053	66.5	3.8	437	2	H69952	hypothetical prote
981	67	3.8	392	2	S72436	hypothetical protei	1054	66.5	3.8	456	2	S61971	hypothetical prote
982	67	3.8	396	2	T27946	kappa-carraghenase	1055	66.5	3.8	463	2	A44808	cellulase (EC 3.2.
983	67	3.8	397	2	I39507	phospholipase C (E	1056	66.5	3.8	477	1	KCHUS1	stromelysin 1 (EC
984	67	3.8	398	2	A30565	3-oxoacyl-(acyl ca	1057	66.5	3.8	519	2	B84539	dihydrofolate redu
985	67	3.8	420	2	AH2711	hypothetical prote	1058	66.5	3.8	525	2	C98183	mannitol 2-dehydro
986	67	3.8	427	2	T04823	fibrinogen gamma c	1059	66.5	3.8	528	1	PAHUI	alkaline phosphata
987	67	3.8	432	1	FGLMGS	acid phosphatase (	1060	66.5	3.8	548	2	C82698	electron transfer
988	67	3.8	437	2	T49034	probable membrane	1061	66.5	3.8	564	2	T41503	alpha-amylase - fi
989	67	3.8	441	2	S60247	platelet-activatin	1062	66.5	3.8	579	2	S33759	alpha,alpha-trehal
990	67	3.8	437	2	S67679	3-oxoacyl-acyl car	1063	66.5	3.8	600	2	T46880	succinate dehydrog
991	67	3.8	441	2	S60247	beta-galactosidas	1064	66.5	3.8	633	2	A75069	dipeptide transpor
992	67	3.8	448	2	JW0038	alpha-galactosidas	1065	66.5	3.8	642	2	A96560	hypothetical prote
993	67	3.8	471	2	S50310	probable porin PA4	1066	66.5	3.8	663	1	QREIC	colicin I receptor
994	67	3.8	484	2	A83082	cyclin-dependent k	1067	66.5	3.8	683	2	S01433	repressor protein
995	67	3.8	496	2	JC5110	chitinase (EC 3.2.	1068	66.5	3.8	705	2	T01730	hypothetical prote
996	67	3.8	499	2	S04856	hypothetical prote	1069	66.5	3.8	714	2	D85014	hypothetical prote
997	67	3.8	509	2	A84404	hypothetical prote	1070	66.5	3.8	730	2	B87266	TonB-dependent rec
998	67	3.8	512	2	T13330	hypothetical prote	1071	66.5	3.8	767	2	C71909	iron (III) dicitra
999	67	3.8	551	2	A83889	hypothetical prote	1072	66.5	3.8	783	2	E89551	probable low-affin
1000	67	3.8	555	2	C97612	hypothetical prote	1073	66.5	3.8	796	2	T37330	glucan endo-1,3-be
1001	67	3.8	560	1	HMIVTW	hemagglutinin prec	1074	66.5	3.8	877	2	JN0772	aconitase Xf0290 [
1002	67	3.8	564	1	HMIVF6	hemagglutinin prec	1075	66.5	3.8	908	2	G82824	probable outer mem
1003	67	3.8	598	2	AG0890	probable arylsulfa	1076	66.5	3.8	970	2	F87450	TonB-dependent rec
1004	67	3.8	634	2	T18711	hypothetical prote	1077	66.5	3.8	1016	2	H71460	ras GTPase-activat
1005	67	3.8	634	2	T18702	hypothetical prote	1078	66.5	3.8	1137	2	D89610	hypothetical prote
1006	67	3.8	651	2	E86242	hypothetical prote	1079	66.5	3.8	1206	2	A64207	neural cell adhesi
1007	67	3.8	656	2	T03473	acetate-CoA ligase	1080	66.5	3.8	1259	2	T19043	ras GTPase-activat
1008	67	3.8	683	2	AB0217	oligopeptidase B (	1081	66.5	3.8	1265	1	A37967	TagA-related prote
1009	67	3.8	693	2	AE0969	ATP-dependent DNA	1082	66.5	3.8	1335	2	A82494	hypothetical prote
1010	67	3.8	694	2	JC6554	complement subcomp	1083	66.5	3.8	1377	2	D90538	probable membrane
1011	67	3.8	699	2	H71005	hypothetical prote	1084	66.5	3.8	1609	2	S25345	hypothetical prote
1012	67	3.8	702	2	A61619	aryphorin precurs	1085	66.5	3.8	1619	2	S67083	hypothetical prote
1013	67	3.8	712	1	YSHUT	threonine-tRNA lig	1086	66.5	3.8	1829	2	T14280	RW1 protein - mous
1014	67	3.8	714	2	D65047	ribonucleoside-dip	1087	66.5	3.8	1876	2	C70749	probable ppsa prot
1015	67	3.8	745	2	T07184	subtilisin-like pr	1088	66.5	3.8	1928	2	J50610	beta-galactosidase
1016	67	3.8	764	2	S48521	AKR1 protein - yea	1089	66.5	3.8	2013	2	A11489	probable peptidogl
1017	67	3.8	788	2	S53923	probable membrane	1090	66.5	3.8	2168	2	D88131	protein F10G7.10 [
1018	67	3.8	931	2	A49737	dipeptidyl aminope	1091	66	3.8	126	2	PH1418	Ig heavy chain V r
1019	67	3.8	983	2	A81723	polymorphic membra	1092	66	3.8	167	2	AH2963	conserved hypothet
1020	67	3.8	1217	2	F97177	alpha-glucosidase	1093	66	3.8	173	2	E98319	hypothetical prote
1021	67	3.8	1376	2	S63986	collagen alpha 5 c	1094	66	3.8	197	2	S25088	dehydrin DHN1 - ga
1022	67	3.8	1388	2	T00063	hypothetical prote	1095	66	3.8	215	2	JC1231	beta-crystallin A3
1023	67	3.8	1451	2	D64203	DNA polymerase III	1096	66	3.8	227	2	S43919	endo-1,4-beta-xyla
1024	67	3.8	2014	2	T21560	hypothetical prote	1097	66	3.8	248	2	PL0038	opacity protein D
1025	66.5	3.8	191	2	G90966	hypothetical prote	1098	66	3.8	253	2	A71648	pseudouridylate sy
1026	66.5	3.8	202	2	S35259	pyruvate decarboxy	1099	66	3.8	259	2	T14722	hypothetical prote
1027	66.5	3.8	205	2	T04370	perml protein - ba	1100	66	3.8	264	2	T46335	hypothetical prote
1028	66.5	3.8	257	2	AB2159	glucose-1-P cytidy	1101	66	3.8	286	2	T02119	probable DnaJ prot
1029	66.5	3.8	261	2	T31741	hypothetical prote	1102	66	3.8	299	2	S32896	hypothetical prote
1030	66.5	3.8	262	2	T50660	alpha-expansin 2 [	1103	66	3.8	314	2	T46276	hypothetical prote
1031	66.5	3.8	270	1	A64367	pyruvate synthase	1104	66	3.8	346	2	T20620	hypothetical prote
1032	66.5	3.8	277	2	S65069	chitinase (EC 3.2.	1105	66	3.8	357	1	S33321	glutamyl endopepti
1033	66.5	3.8	278	2	S39310	merozoite surface	1106	66	3.8	370	2	S61058	probable p-loop AT
1034	66.5	3.8	311	2	C89968	leukotoxin LukE [i	1107	66	3.8	377	2	JC7535	glutamate-ammonia
1035	66.5	3.8	319	2	T17438	protein regulator	1108	66	3.8	405	2	G75027	chitinase (EC 3.2.
1036	66.5	3.8	319	2	AD0233	transcription regu	1109	66	3.8	416	2	D75027	alanyl-tRNA synthe
1037	66.5	3.8	354	2	T05975	probable carboxy-t	1110	66	3.8	417	2	S76588	hypothetical prote
1038	66.5	3.8	359	2	F72418	basic membrane pro	1111	66	3.8	422	2	H70481	hemolysin homolog
1039	66.5	3.8	362	2	A38135	ADP-ribosylarginin	1112	66	3.8	433	2	T48118	peptide ABC transp
1040	66.5	3.8	362	2	T00086	rgpAc protein - St	1113	66	3.8	440	2	G90936	hypothetical prote
1041	66.5	3.8	367	2	A83321	probable periplasm	1114	66	3.8	440	2	C85785	probable thiosulfa
1042	66.5	3.8	370	2	H83541	probable oxidoredu	1115	66	3.8	445	2	A27263	50K spicule matrix
1043	66.5	3.8	375	2	A39293	cytotoxic granule-	1116	66	3.8	485	2	S36772	E-selectin - bovin
1044	66.5	3.8	378	2	T11713	probable alpha-1,2	1117	66	3.8	499	2	JC6141	beta 1,3-glucanase
1045	66.5	3.8	398	2	F75417	glutamate dehydr	1118	66	3.8	503	2	T39216	aldehyde dehydroge
1046	66.5	3.8	399	1	AJFF1M	L-sorbose ammonia	1119	66	3.8	503	2	AC2446	hypothetical prote
1047	66.5	3.8	400	2	A42237	fork head domain p	1120	66	3.8	516	2	JE0134	cysteine proteinas
1048	66.5	3.8	400	2	A46297	beta-1,6-N-acetyl	1121	66	3.8	527	2	A81712	mannan endo-1,4-be
1049	66.5	3.8	405	2	H86249	hypothetical prote	1122	66	3.8				
1050	66.5	3.8	406	2	A41734	beta-galactoside a	1123	66	3.8				
1051	66.5	3.8	418	2	C98110	tyrosine-tRNA liga	1124	66	3.8				

1125	66	3.8	527	2	T39927	probable serine-ri	1198	65.5	3.7	360	2	S00834	int-1-like protein
1126	66	3.8	529	2	T35966	probable secreted	1199	65.5	3.7	363	2	D83566	hypothetical prote
1127	66	3.8	530	2	JC7979	cellobiohydrolase	1200	65.5	3.7	365	2	JC4027	glutamate-ammonia
1128	66	3.8	532	2	A82551	phage-related port	1201	65.5	3.7	367	1	S62746	alcohol dehydrogen
1129	66	3.8	539	2	C90789	hemolysin activato	1202	65.5	3.7	397	2	JW0075	cysteine-dependent
1130	66	3.8	539	2	F85649	hemolysin activato	1203	65.5	3.7	405	2	T35117	probable secreted
1131	66	3.8	555	2	T06491	beta-fructofuranos	1204	65.5	3.7	406	2	T36632	probable oxidoredu
1132	66	3.8	556	2	T39476	probable serine-ri	1205	65.5	3.7	410	2	G81651	conserved hypothet
1133	66	3.8	574	2	T40213	hypothetical prote	1206	65.5	3.7	417	2	A96610	probable pectinase
1134	66	3.8	582	2	T06380	beta-fructofuranos	1207	65.5	3.7	434	2	T04248	hypothetical prote
1135	66	3.8	600	2	S56744	mucin (clone pGM7-	1208	65.5	3.7	436	2	T39855	beta-transducin -
1136	66	3.8	622	2	T01414	starch synthase (E	1209	65.5	3.7	456	2	T40416	hypothetical prote
1137	66	3.8	623	2	I64034	hypothetical prote	1210	65.5	3.7	469	1	H84669	acid phosphatase (
1138	66	3.8	652	2	S47979	aliB protein precu	1211	65.5	3.7	482	1	A34671	triacylglycerol li
1139	66	3.8	656	2	AE1479	probable cell surf	1212	65.5	3.7	488	2	T21701	hypothetical prote
1140	66	3.8	661	2	S49901	coat protein gp1 -	1213	65.5	3.7	497	2	H83886	hypothetical prote
1141	66	3.8	686	2	A59348	formate dehydrogen	1214	65.5	3.7	502	2	T20130	hypothetical prote
1142	66	3.8	689	2	S66006	conserved hypothet	1215	65.5	3.7	513	2	S58200	probable membrane
1143	66	3.8	704	2	T13665	NADH2 dehydrogenas	1216	65.5	3.7	521	1	HYBSN	bacillolysin (EC 3
1144	66	3.8	711	2	C87597	alpha-glucuronidas	1217	65.5	3.7	534	1	VCWWSF	env polyprotein -
1145	66	3.8	713	2	D85503	lysine decarboxyla	1218	65.5	3.7	535	2	T47790	hypothetical prote
1146	66	3.8	713	2	D90652	lysine decarboxyla	1219	65.5	3.7	551	2	H86121	trehalase 6-P hydr
1147	66	3.8	713	2	B64743	lysine decarboxyla	1220	65.5	3.7	551	2	H91280	trehalase 6-P hydr
1148	66	3.8	732	2	T44483	receptor-like prot	1221	65.5	3.7	554	2	F90462	sugar-binding peri
1149	66	3.8	741	2	D81798	lactoferrin-bindin	1222	65.5	3.7	584	1	ALBY	alpha-glucosidase
1150	66	3.8	776	2	A55448	Ah receptor nuclea	1223	65.5	3.7	584	2	S64627	alpha-glucosidase
1151	66	3.8	777	2	G69310	penicillin G acyla	1224	65.5	3.7	584	2	S46183	alpha-glucosidase
1152	66	3.8	778	2	AI3064	glucose dehydrogen	1225	65.5	3.7	591	2	G96592	probable beta-fruc
1153	66	3.8	778	2	G98221	glucose dehydrogen	1226	65.5	3.7	607	2	H88065	protein T16A1.1 [i
1154	66	3.8	779	2	AE2402	alpha-glucosidase	1227	65.5	3.7	608	2	JQ1462	phosphoenolpyruvat
1155	66	3.8	784	2	T13579	hypothetical prote	1228	65.5	3.7	617	2	T15408	hypothetical prote
1156	66	3.8	799	2	T01663	1,4-alpha-glucan b	1229	65.5	3.7	620	1	UYPVAP	noncapsid protein
1157	66	3.8	846	2	A86663	aminopeptidase N l	1230	65.5	3.7	622	2	F71174	hypothetical prote
1158	66	3.8	886	2	A59223	nitrate reductase	1231	65.5	3.7	625	2	T06184	sucrose-fructan 6-
1159	66	3.8	893	2	E95053	cell wall surface	1232	65.5	3.7	627	2	S14683	Ig mu chain precur
1160	66	3.8	902	2	A60560	formyltetrahydrofo	1233	65.5	3.7	637	2	T13432	gamma-glutamyltran
1161	66	3.8	912	2	F71433	probable growth re	1234	65.5	3.7	642	1	SYECTT	threonine-tRNA lig
1162	66	3.8	940	2	S49087	lactoferrin bindin	1235	65.5	3.7	642	2	B90932	threonine tRNA syn
1163	66	3.8	958	1	JN0102	glucan 1,4-alpha-g	1236	65.5	3.7	642	2	F85780	threonine tRNA syn
1164	66	3.8	980	2	H90681	probable flagellin	1237	65.5	3.7	642	2	AB0297	threonine-tRNA lig
1165	66	3.8	1024	2	H87599	TonB-dependent rec	1238	65.5	3.7	648	2	S71885	sex-determining pr
1166	66	3.8	1036	2	S73601	protein P200 - Myc	1239	65.5	3.7	652	2	E90505	hypothetical prote
1167	66	3.8	1166	2	T15628	hypothetical prote	1240	65.5	3.7	681	2	E83636	oligopeptidase A P
1168	66	3.8	1180	2	T31066	vascular cadherin-	1241	65.5	3.7	702	2	T12677	NADH2 dehydrogenas
1169	66	3.8	1289	1	GUBPT4	proximal tail fibe	1242	65.5	3.7	713	2	AE0531	lysine decarboxyla
1170	66	3.8	1360	2	T33922	hypothetical prote	1243	65.5	3.7	728	1	NQECA	1,4-alpha-glucan b
1171	66	3.8	1385	2	D89824	hypothetical prote	1244	65.5	3.7	730	2	JH0798	fasciclin IV precu
1172	66	3.8	1426	2	E90456	oxydoreductase, pr	1245	65.5	3.7	759	2	E84538	hypothetical prote
1173	66	3.8	1584	2	T18276	protein-tyrosine k	1246	65.5	3.7	770	2	S60676	cellobiose oxidase
1174	66	3.8	1948	2	B69511	N conserved hypoth	1247	65.5	3.7	782	2	A61625	tenascin-like prot
1175	66	3.8	2185	1	GNNYB3	genome polyprotein	1248	65.5	3.7	790	2	S61587	transcription acti
1176	66	3.8	2204	2	A70524	probable ppg prote	1249	65.5	3.7	792	2	AD0104	probable glucosida
1177	66	3.8	2228	2	T14029	variant-specific s	1250	65.5	3.7	814	2	S19658	microbial collagen
1178	66	3.8	4543	1	A53102	alpha-2-macroglubu	1251	65.5	3.7	815	2	C71810	type I restriction
1179	66	3.8	4544	1	S02392	alpha-2-macroglubu	1252	65.5	3.7	838	2	T20125	hypothetical prote
1180	66	3.8	4545	1	S25111	alpha-2-macroglubu	1253	65.5	3.7	844	2	B83136	probable fimbrial
1181	65.5	3.7	189	2	A36846	I2R protein - vari	1254	65.5	3.7	891	2	A82755	beta-mannosidase p
1182	65.5	3.7	189	2	T28523	hypothetical prote	1255	65.5	3.7	903	2	A87704	aconitate hydratase
1183	65.5	3.7	189	2	C72161	J2R protein - vari	1256	65.5	3.7	910	2	B83451	aconitate hydratase
1184	65.5	3.7	191	2	G85814	probable outer mem	1257	65.5	3.7	1015	2	T15830	hypothetical prote
1185	65.5	3.7	230	2	I50097	MHC class II beta	1258	65.5	3.7	1020	2	D83679	hypothetical prote
1186	65.5	3.7	245	2	E71948	probable outer mem	1259	65.5	3.7	1041	2	T31437	integrin alpha cha
1187	65.5	3.7	255	2	AC0384	probable exported	1260	65.5	3.7	1054	2	T30933	chitinase (EC 3.2.
1188	65.5	3.7	273	2	T42146	hypothetical prote	1261	65.5	3.7	1072	2	A38457	integrin alpha-6 c
1189	65.5	3.7	279	2	T00225	hypothetical prote	1262	65.5	3.7	1078	2	F97907	hyaluronate lyase
1190	65.5	3.7	293	2	JQ0380	proteinase T (EC 3	1263	65.5	3.7	1097	2	T40678	hypothetical prote
1191	65.5	3.7	311	2	G86324	hypothetical prote	1264	65.5	3.7	1157	2	F97255	fusion of alpha-gl
1192	65.5	3.7	326	2	S26216	glutamate-ammonia	1265	65.5	3.7	1177	2	A36984	protein-tyrosine k
1193	65.5	3.7	327	2	D82678	transcription regu	1266	65.5	3.7	1345	2	S55669	tegument protein 7
1194	65.5	3.7	338	2	S65535	light-harvesting c	1267	65.5	3.7	1567	2	S11672	ice nucleation pro
1195	65.5	3.7	341	2	JQ1189	CbHE protein - Cox	1268	65.5	3.7	1609	2	T01797	hypothetical prote
1196	65.5	3.7	357	2	T20659	hypothetical prote	1269	65.5	3.7	1627	2	S65464	pregnancy-associat
1197	65.5	3.7	359	1	A31425	uracil-DNA glycosy	1270	65.5	3.7	1657	2	T25421	hypothetical prote



1271	65.5	3.7	1778	2	T50074	probable nucleopor	1344	65	3.7	749	2	A45687	outer capsid prote
1272	65.5	3.7	1939	2	D97316	probable S-layer p	1345	65	3.7	760	2	D69865	conserved hypothet
1273	65.5	3.7	2232	2	T34434	hypothetical prote	1346	65	3.7	763	2	S23457	polysulfide reduct
1274	65.5	3.7	2543	2	T31687	surface antigen - p	1347	65	3.7	773	2	JE0387	exo-alpha-sialidas
1275	65	3.7	121	2	A49590	Ig heavy chain V r	1348	65	3.7	791	2	A56241	aryl hydrocarbon r
1276	65	3.7	133	2	C33548	Ig heavy chain V-1	1349	65	3.7	800	2	AD3129	conserved hypothet
1277	65	3.7	144	2	AB3029	hypothetical prote	1350	65	3.7	815	2	E98158	hypothetical prote
1278	65	3.7	191	2	G65017	hypothetical prote	1351	65	3.7	837	2	S36713	CCR4 protein - yea
1279	65	3.7	226	2	T46058	porin-like protein	1352	65	3.7	838	2	H82939	conserved hypothet
1280	65	3.7	247	1	Q0BEF1	HLF3 protein prec	1353	65	3.7	875	2	T12794	hypothetical yomG
1281	65	3.7	254	1	HLHUD7	MHC class II histo	1354	65	3.7	878	2	S74207	lipoxigenase (EC 1
1282	65	3.7	258	2	T10083	expansin S2 precu	1355	65	3.7	879	2	D96804	unknown protein T5
1283	65	3.7	280	2	T29200	hypothetical prote	1356	65	3.7	904	2	AH2019	hypothetical prote
1284	65	3.7	285	2	S74771	hypothetical prote	1357	65	3.7	905	1	A27410	nucleotide diphosp
1285	65	3.7	294	2	S49152	hypothetical prote	1358	65	3.7	932	2	AB0003	Me12-like protein
1286	65	3.7	296	2	T03683	nucleoside-specifi	1359	65	3.7	966	2	H97717	DNA-directed DNA p
1287	65	3.7	320	2	T16823	peroxidase (EC 1.1	1360	65	3.7	1070	2	S75712	hypothetical prote
1288	65	3.7	322	2	T03686	hypothetical prote	1361	65	3.7	1104	2	A60999	cellulase (EC 3.2.
1289	65	3.7	324	2	A39889	peroxidase (EC 1.1	1362	65	3.7	1136	2	T30878	alpha-amylase (EC
1291	65	3.7	342	2	S14432	heterogeneous ribo	1363	65	3.7	1148	2	T18770	dynein heavy chain
1292	65	3.7	344	2	E96021	F19K19.12 protein	1364	65	3.7	1172	1	TSHUP2	probable calcium c
1293	65	3.7	363	2	S30386	probable glutamate	1365	65	3.7	1301	1	A41622	thrombospondin 2 p
1294	65	3.7	370	2	T48578	mannan endo-1,4-be	1366	65	3.7	1367	1	IGHUR1	protein-tyrosine-p
1295	65	3.7	373	2	C81689	hypothetical prote	1367	65	3.7	1398	2	H90698	insulin-like growt
1296	65	3.7	376	2	E84742	tRNA (5-methylamin	1368	65	3.7	1400	2	E90886	RhSD core protein
1297	65	3.7	380	1	TVFVMM	hypothetical prote	1369	65	3.7	1445	1	A48148	hypothetical prote
1298	65	3.7	384	2	T37232	protein kinase (EC	1370	65	3.7	2083	2	T18397	RhSe core protein
1299	65	3.7	389	2	B42708	secreted beta-mann	1371	65	3.7	2098	2	T42721	protein-tyrosine-p
1300	65	3.7	390	2	T14794	serine-type D-Ala-	1372	65	3.7	2248	2	A35938	CRP-ductin-alpha p
1301	65	3.7	400	2	T19517	hypothetical prote	1373	65	3.7	2366	2	A57096	probable exported
1302	65	3.7	404	2	AH2303	hypothetical prote	1374	65	3.7	2616	2	S10317	profilaggrin - hum
1303	65	3.7	404	2	H86128	hypothetical prote	1375	65	3.7	3507	2	T34513	toxin B - Clostrid
1304	65	3.7	404	2	E91287	hypothetical prote	1376	65	3.7	4660	2	T42737	nudel protein prec
1305	65	3.7	415	2	T44436	hypothetical prote	1377	65	3.7	130	1	WMWGN2	hypothetical prote
1306	65	3.7	416	2	T02194	3-oxoacyl-[acyl-ca	1378	65	3.7	151	2	T15428	gp330 protein prec
1307	65	3.7	429	1	AJFBQD	probable pectinace	1379	65	3.7	165	2	A47148	14K protein - narc
1308	65	3.7	451	2	JE0313	glutamate-ammonia	1380	65	3.7	180	2	S42433	hypothetical prote
1309	65	3.7	455	2	F64617	exoglucanase (EC 3	1381	64.5	3.7	196	2	JQ1078	reg I, regeneratin
1310	65	3.7	457	2	S63608	hypothetical prote	1382	64.5	3.7	209	2	T12075	TDP-deoxyglucose e
1311	65	3.7	480	2	AB0148	glutamate dehydrog	1383	64.5	3.7	254	2	D64560	styler glycoprotei
1312	65	3.7	487	2	D95887	catalase (EC 1.11.	1384	64.5	3.7	268	1	KONH2C	ribonuclease (EC 3
1313	65	3.7	502	2	A70582	probable aldehyde	1385	64.5	3.7	273	2	AC1483	outer membrane pro
1314	65	3.7	507	2	A40659	hypothetical prote	1386	64.5	3.7	274	2	T30588	opacity protein p.
1315	65	3.7	519	2	I64163	elastase (EC 3.4.2	1387	64.5	3.7	280	2	JC7852	B. subtilis IolB p
1316	65	3.7	523	2	B95922	hypothetical prote	1388	64.5	3.7	297	1	S70988	hypothetical prote
1317	65	3.7	532	2	C97228	hypothetical nucle	1389	64.5	3.7	302	2	S50579	chitosanase (EC 3.
1318	65	3.7	537	2	T29567	probable peptide A	1390	64.5	3.7	323	2	T02617	gnd protein - Myco
1319	65	3.7	547	2	S30929	hypothetical prote	1391	64.5	3.7	324	2	T09873	hypothetical prote
1320	65	3.7	588	2	B83457	catechol oxidase (	1392	64.5	3.7	326	1	C41335	probable cellulase
1321	65	3.7	591	2	A35847	glyoxylate carboli	1393	64.5	3.7	326	1	B72278	microbial serine p
1322	65	3.7	595	2	AB0818	Fos-related antige	1394	64.5	3.7	329	1	AJZJQ2	conserved hypothet
1323	65	3.7	601	2	T11677	transferrin-bindin	1395	64.5	3.7	330	2	D96787	glutamate-ammonia
1324	65	3.7	614	1	QRECBT	probable transcrip	1396	64.5	3.7	331	2	A96621	protein T4O12.3 [i
1325	65	3.7	624	2	G82508	vitamin b12 recept	1397	64.5	3.7	342	2	T18819	probable heat shoc
1326	65	3.7	634	2	T41319	hypothetical prote	1398	64.5	3.7	358	2	S15908	hypothetical prote
1327	65	3.7	639	2	S23118	conserved hypothet	1399	64.5	3.7	359	2	F89075	site-specific DNA-
1328	65	3.7	640	2	S23008	proprotein convert	1400	64.5	3.7	365	1	MMECNC	protein K04A8.1 [i
1329	65	3.7	650	2	T06648	insulin-like growt	1401	64.5	3.7	382	2	T27076	outer membrane por
1330	65	3.7	652	2	G95177	hypothetical prote	1402	64.5	3.7	391	2	AI3375	hypothetical prote
1331	65	3.7	652	2	B98044	hypothetical prote	1403	64.5	3.7	397	2	A75503	glutamate-ammonia
1332	65	3.7	654	2	B75587	hypothetical prote	1404	64.5	3.7	407	2	T21956	rare lipoprotein A
1333	65	3.7	664	2	F83376	probable N-glycosyl	1405	64.5	3.7	409	2	F83899	hypothetical prote
1334	65	3.7	667	2	T33526	conserved glycosyl	1406	64.5	3.7	414	2	T44513	hypothetical prote
1335	65	3.7	668	2	E71879	hypothetical prote	1407	64.5	3.7	416	2	G72305	hypothetical prote
1336	65	3.7	678	2	T05821	probable outer mem	1408	64.5	3.7	421	2	S10514	glutamate dehydrog
1337	65	3.7	681	2	T33381	hypothetical prote	1409	64.5	3.7	421	2	G95308	glutamate dehydrog
1338	65	3.7	681	2	G87276	hypothetical prote	1410	64.5	3.7	427	1	KGHUL1	alpha-amylase (EC
1339	65	3.7	687	2	D83547	hypothetical prote	1411	64.5	3.7				kininogen, LMW pre
1340	65	3.7	697	2	T13370	hypothetical prote	1412	64.5	3.7				
1341	65	3.7	702	2	AH0625	NADH2 dehydrogenas	1413	64.5	3.7				
1342	65	3.7	705	2	T00975	conserved hypothet	1414	64.5	3.7				
1343	65	3.7	717	2	H85171	hypothetical prote	1415	64.5	3.7				
						DEF (ClA1) protein	1416	64.5	3.7				

1417 64.5 3.7 440 2 AF1472  
1418 64.5 3.7 442 1 E69997  
1419 64.5 3.7 454 2 D69177  
1420 64.5 3.7 468 2 A70065  
1421 64.5 3.7 471 2 T30265  
1422 64.5 3.7 476 2 A41463  
1423 64.5 3.7 497 2 T15812  
1424 64.5 3.7 499 2 S52422  
1425 64.5 3.7 503 2 G84234  
1426 64.5 3.7 507 2 S15476  
1427 64.5 3.7 513 2 S21535  
1428 64.5 3.7 538 2 A65175  
1429 64.5 3.7 546 2 F70866  
1430 64.5 3.7 558 2 G69126  
1431 64.5 3.7 572 2 G84238  
1432 64.5 3.7 590 2 C88099  
1433 64.5 3.7 631 2 T32761  
1434 64.5 3.7 638 2 T20944  
1435 64.5 3.7 643 2 S55593  
1436 64.5 3.7 644 1 KGHUH1  
1437 64.5 3.7 662 2 T01857  
1438 64.5 3.7 677 2 A27286  
1439 64.5 3.7 680 2 C83029  
1440 64.5 3.7 692 2 A97013  
1441 64.5 3.7 708 2 T00064  
1442 64.5 3.7 712 2 AC1058  
1443 64.5 3.7 725 2 T43092  
1444 64.5 3.7 730 1 I64118  
1445 64.5 3.7 732 2 AB2732  
1446 64.5 3.7 741 2 B97513  
1447 64.5 3.7 741 2 JS0606  
1448 64.5 3.7 776 2 AB2240  
1449 64.5 3.7 825 2 A59296  
1450 64.5 3.7 830 2 T06578  
1451 64.5 3.7 834 2 T39891  
1452 64.5 3.7 898 2 A40114  
1453 64.5 3.7 904 2 T04377  
1454 64.5 3.7 921 2 S35160  
1455 64.5 3.7 947 2 S71922  
1456 64.5 3.7 947 2 T42056  
1457 64.5 3.7 960 2 A41638  
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1459 64.5 3.7 980 2 D85532  
1460 64.5 3.7 990 2 H90703  
1461 64.5 3.7 990 2 C85554  
1462 64.5 3.7 1010 2 I40329  
1463 64.5 3.7 1035 1 A43090  
1464 64.5 3.7 1062 2 F89102  
1465 64.5 3.7 1068 2 S01519  
1466 64.5 3.7 1080 2 T00587  
1467 64.5 3.7 1080 2 T19048  
1468 64.5 3.7 1095 2 PC1114  
1469 64.5 3.7 1142 2 C97080  
1470 64.5 3.7 1170 1 TSHUP1  
1471 64.5 3.7 1181 2 E83658  
1472 64.5 3.7 1200 1 SNPSO  
1473 64.5 3.7 1216 2 T02146  
1474 64.5 3.7 1260 2 A72603  
1475 64.5 3.7 1312 1 A34171  
1476 64.5 3.7 1451 1 JQ1719  
1477 64.5 3.7 1556 2 A60988  
1478 64.5 3.7 1565 2 S04729  
1479 64.5 3.7 1817 2 AD2165  
1480 64 3.7 129 2 A33548  
1481 64 3.7 133 2 AE2202  
1482 64 3.7 138 2 A82022  
1483 64 3.7 167 2 A37246  
1484 64 3.7 169 1 MBBOB  
1485 64 3.7 208 2 T33341  
1486 64 3.7 219 2 S42674  
1487 64 3.7 233 2 A29029  
1488 64 3.7 241 2 S71056  
1489 64 3.7 309 1 S12961

B. subtilis Yych p  
nitrotriacetate  
hypothetical prote  
hypothetical prote  
sugar binding prot  
alkaline metallopr  
hypothetical prote  
chitinase (EC 3.2.  
aldehyde dehydroge  
transmembrane gly  
nitrate reductase  
hypothetical 60.6  
probable maltase -  
acetyl-CoA synthet  
hypothetical prote  
protein F18A12.8 [I  
hypothetical prote  
hypothetical prote  
membrane protein S  
kininogen, HMW pre  
hypothetical prote  
levanase (EC 3.2.1  
hypothetical proue  
hypothetical prote  
hypothetical prote  
ribonucleoside-tri  
probable transfer  
1,4-alpha-glucan b  
conserved hypothet  
homeobox protein A  
type I restriction  
alpha-L-arabinofur  
1,4-alpha-glucan b  
probable integral  
fasciclin II precu  
probable pullulana  
aspartate kinase (  
preprotein translo  
preprotein translo  
chitin synthase (E  
probable secreted  
probable structura  
bacteriophage N4 a  
bacteriophage N4 a  
brkA prtoein - Bor  
enteropeptidase (E  
protein F25E5.1 [i  
hypothetical prote  
probable ubiquitin  
probable Pro-X car  
SKCDC25 protein -  
levanase/invertase  
thrombospondin 1 p  
transcription-repa  
ice nucleation pro  
coatomer complex a  
probable nitrate r  
peptidyl-dipeptida  
E2 glycoprotein pr  
saliva-interacting  
surface antigen pa  
two-component hybr  
Ig heavy chain V-1  
hypothetical prote  
truncated pilin NM  
myelin basic prote  
myelin basic prote  
hypothetical prote  
adhesive protein -  
gag polyprotein -  
major prion protei  
phosphoprotein pho

1490 64 3.7 312 2 JQ1318  
1491 64 3.7 326 1 GOVZML  
1492 64 3.7 326 2 F96522  
1493 64 3.7 335 2 A83193  
1494 64 3.7 339 2 S39979  
1495 64 3.7 340 2 S40414  
1496 64 3.7 365 2 S49007  
1497 64 3.7 366 2 E85729  
1498 64 3.7 366 2 D90888  
1499 64 3.7 376 2 S47986  
1500 64 3.7 376 2 S24408

pectin lyase (EC 4  
T2 protein - myxom  
hypothetical prote  
hypothetical prote  
chitinase (EC 3.2.  
chitinase (EC 3.2.  
actin - Pythium ir  
probable outer mem  
putaive outer memb  
actin-related prot  
actin - Achlya bis

ALIGNMENTS

RESULT 1  
JE0328

intelectin - mouse

C:Species: Mus musculus (house mouse)

C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C:Accession: JE0328

R:Komiya, T.; Tanigawa, Y.; Hirohashi, S.

Biochem. Biophys. Res. Commun. 251, 759-762, 1998

A:Title: Cloning of the novel gene intelectin, which is expressed in intestinal paneth

A:Reference number: JE0328; MUID:99008898; PMID:9790983

A:Accession: JE0328

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-313 <KOM>

A:Cross-references: UNIPROT:O88310; UNIPARC:UPI0000029628; DDBJ:AB016496; NID:G3357908;

Query Match

Best Local Similarity 81.7%; Score 1427; DB 2; Length 313;

Matches 255; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

Qy 1 MNQLSFLLELIATTRGWSSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT 60

Db 1 MTQLGFLLFIMVATRGCSAAEENLDTNRWNSFFSSLPRSCKEIKQHTKAQDGLYFLRT 60

Qy 61 ENGVIYQTFCDMTSGGGWTLVASVHENDMRGKCTVGRWSSQGSKADYPEGDGNWANY 120

Db 61 KNGVIYQTFCDMTTAGGGWTLVASVHENNMKGKCTVGRWSSQGNRADYPEGDGNWANY 120

Qy 121 NTFGSABAATSDDYKNPGYYDIOAKDLGIWHVPNKS PMQHWNSLLRYRTDTGFLQITLG 180

Db 121 NTFGSABAATSDDYKNPGYFDIOAENLGIWHVPNKS PLHNWRKSSLLRYRTFTGFLQHLG 180

Qy 181 HNLFGIYQKYPVKYGEKCKWTNDNGPVPVYDFGDAQKTASYSPYQGREFTAGVQFRV 240

Db 181 HNLFLYKYPVKYGEKCKWTNDNGPALPVYDFGDARKTASYSPSQGREFTAGVQFRV 240

Qy 241 FNNERAANALCAGMRVTGCMTEHHCIGGGYFPEASPOQCQDFSGFDWSGYGTHVGYSSS 300

Db 241 FNNERAASALCAGVRVTGCMTEHHCIGGGGFFPEGNPVQCQDFASFDWDGYGTHNGYSSS 300

Qy 301 REITEAAVLLFYR 313

Db 301 RKITEAAVLLFYR 313

RESULT 2

S49589

cortical granule lectin - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 05-Mar-1995 #sequence\_revision 12-May-1995 #text\_change 09-Jul-2004

C:Accession: S49589

R:Chang, B.Y.; Wardrip, N.J.; Hedrick, J.L.

submitted to the EMBL Data Library, November 1994

A:Description: Molecular cloning and characterization of cortical granule lectin: an es

A:Reference number: S49589

A:Accession: S49589

A>Status: preliminary







A;Gene: slyD; Cj0115

Query Match		6.0%;	Score 105.5;	DB 2;	Length 189;
Best Local Similarity		28.9%;	Pred. No. 0.28;		
Matches		37;	Conservative	15;	Mismatches 45; Indels 31; Gaps 8;
QY	172	DTGFLQTLGHNLF-GIYQKYPVK-YGEGKCWTDNGPVPV-VYDFGDAQKTASYSPYQG	228		
Db	73	DENAVQTLPKEQFAGIDLKVGMELFEG-----ENGETVRVTVKEIGENDVTIDYNHPYAG	128		
QY	229	RE--FTAGFVQFRVFNNERAANALCAGMRVTGCNT-----EHH-----CIGGGGYFP	273		
Db	129	RDLLFSLNIVDARAASEDEILTGIAGSHSCGCGSGHGHDDHHGHGCGGCCGGG---	185		
QY	274	EASPPQCG	281		
Db	186	-----CG	187		

RESULT 7  
T32131  
hypothetical protein R07C3.12 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T32131  
R;Lamar, B.; Kramer, J.  
submitted to the EMBL Data Library, July 1997  
A;Description: The sequence of C. elegans cosmid R07C3.  
A;Reference number: Z21125  
A;Accession: T32131  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-616 <LAM>  
A;Cross-references: UNIPROT:O16770; UNIPARC:UPI00000828BB; EMBL:AF016686; PIDN:AAB66241.  
A;Experimental source: strain Bristol N2; clone R07C3  
C;Genetics:  
A;Gene: CESP:R07C3.12  
A;Map position: 2  
A;Introns: 47/1; 81/3; 112/3; 358/3; 438/1; 519/3

Query Match		6.0%;	Score 105.5;	DB 2;	Length 616;
Best Local Similarity		21.5%;	Pred. No. 1.1;		
Matches		70;	Conservative	43;	Mismatches 133; Indels 79; Gaps 16;
QY	17	W-STDEANTY-FKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT----ENGVIQ---	67		
Db	34	WVSADDFSQFRYISTTAAISTRAPATTPAAGRCPCAGSSSLNDITCVKLFDTPTMIFQGAN	93		
QY	68	TFCDMTSGGGGWTLVASVHEND-----MRGKCT--VGDRWSSQQGSKADYPEGDGNW	117		
Db	94	LVCRNISGGNGLVSIHSAEDNTALLNALNNKTKTIWGLTQCSPSPSCSEWTDGSGTT	153		
QY	118	ANYNTFGSAEATSDDYKNP-----GYVDIQAKOLGIWHVPNKSPMQHWRNSSLLRYRTD	172		
Db	154	SNYNNFTSG-----YPKPVRGPRGYMWALGSDIGKNF-----SSDEDYSTH	194		
QY	173	TGFLQTLGHNLFGIYQKYPVKYGEKWCWTDNGPVPVYDFGDAQKTASY-YSPYQOREF	231		
Db	195	SFFCEV-----PKSSNVSAETPLILIFHFCYSVNTYLLSEPDAREF	236		
QY	232	TAGFVQFRVFNNERAAN-----ALCAGMRV-----TGCNTEHHCIGGGGYFPEASPPQCGDF	283		
Db	237	CLSLEDLVSIHSAQENDFIQSLSISNTVIDEFTGAATD----GVGKYWVDGS---FFDY	289		
QY	284	SGFDWSGYGTHVGYSSSRREITAAV	308		
Db	290	SNFGY--FGTNLGKCSLSMSGSVV	312		

RESULT 8  
FNBO  
fibronectin - bovine  
C;Species: Bos primigenius taurus (cattle)

C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004  
C;Accession: A26452; B21165; A23292  
R;Skorstengaard, K.; Jensen, M.S.; Sahl, P.; Petersen, T.E.; Magnusson, S.  
Eur. J. Biochem. 161, 441-453, 1986  
A;Title: Complete primary structure of bovine plasma fibronectin.  
A;Reference number: A26452; MUID:87054047; PMID:3780752  
A;Accession: A26452  
A;Molecule type: protein  
A;Residues: 1-2265 <SKO>  
A;Cross-references: UNIPROT:P07589; UNIPARC:UPI000012A7BE  
R;Kornblitt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.  
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983  
A;Title: Isolation and characterization of cDNA clones for human and bovine fibronectin  
A;Reference number: A21165; MUID:83221567; PMID:6304699  
A;Accession: B21165  
A;Molecule type: mRNA  
A;Residues: 2170-2265 <KOR>  
A;Cross-references: UNIPARC:UPI000016C30C; GB:K00800; NID:G163055; PIDN:AAA30521.2; PI=  
R;Petersen, T.E.; Thogersen, H.C.; Skorstengaard, K.; Vibe-Pedersen, K.; Sahl, P.; Sot=  
Proc. Natl. Acad. Sci. U.S.A. 80, 137-141, 1983  
A;Title: Partial primary structure of bovine plasma fibronectin: three types of interna=  
A;Reference number: A23292; MUID:83117805; PMID:6218503  
A;Accession: A23292  
A;Molecule type: protein  
A;Residues: 1-16, 'C', 18-20, 'S', 22-432; 447-463; 1367-1517; 1567-1673; 2062-2176, 'N', 2178-22  
A;Cross-references: UNIPARC:UPI000017433E; UNIPARC:UPI000017433F; UNIPARC:UPI0000174340  
C;Comment: Cys-1201 and Cys-2015 have free sulphydryl groups.  
C;Comment: The plasma fibronectin molecule consists of two chains, which are connected =  
aling, and maintenance of cell shape.  
C;Comment: Plasma fibronectin is synthesized by hepatocytes.  
C;Superfamily: fibronectin; fibronectin type I repeat homology <1F1>  
C;Keywords: acute phase; alternative splicing; collagen binding; duplication; extracell=  
F;21-241/Domain: fibrin and heparin binding <FBR>  
F;21-56/Domain: fibronectin type I repeat homology <1F1>  
F;66-104/Domain: fibronectin type I repeat homology <1F2>  
F;110-148/Domain: fibronectin type I repeat homology <1F3>  
F;155-194/Domain: fibronectin type I repeat homology <1F4>  
F;200-239/Domain: fibronectin type I repeat homology <1F5>  
F;277-577/Domain: collagen binding <CBR>  
F;277-311/Domain: fibronectin type I repeat homology <1F6>  
F;329-370/Domain: fibronectin type II repeat homology <2F1>  
F;389-430/Domain: fibronectin type II repeat homology <2F2>  
F;439-477/Domain: fibronectin type I repeat homology <1F7>  
F;487-524/Domain: fibronectin type I repeat homology <1F8>  
F;530-568/Domain: fibronectin type I repeat homology <1F9>  
F;578-661/Domain: fibronectin type III repeat homology <FN3A>  
F;688-770/Domain: fibronectin type III repeat homology <FN3B>  
F;779-860/Domain: fibronectin type III repeat homology <FN3C>  
F;875-957/Domain: fibronectin type III repeat homology <FN3D>  
F;965-1046/Domain: fibronectin type III repeat homology <FN3E>  
F;1055-1134/Domain: fibronectin type III repeat homology <FN3F>  
F;1142-1227/Domain: fibronectin type III repeat homology <FN3G>  
F;1235-1318/Domain: fibronectin type III repeat homology <FN3H>  
F;1326-1404/Domain: fibronectin type III repeat homology <GN3I>  
F;1410-1517/Domain: cell attachment <CAD>  
F;1416-1502/Domain: fibronectin type III repeat homology <FN3J>  
F;1493-1495/Region: cell attachment (R-G-D) motif  
F;1510-1592/Domain: fibronectin type III repeat homology <FN3K>  
F;1600-1870/Domain: heparin binding <HB2>  
F;1600-1682/Domain: fibronectin type III repeat homology <FN3L>  
F;1692-1773/Domain: fibronectin type III repeat homology <FN3M>  
F;1781-1863/Domain: fibronectin type III repeat homology <FN3N>  
F;1970-1972/Region: cell attachment (R-G-D) motif  
F;1982-2062/Domain: fibronectin type III repeat homology <FN3O>  
F;1985-2216/Domain: fibrin binding <FB2>  
F;2085-2124/Domain: fibronectin type I repeat homology <1F10>  
F;2130-2167/Domain: fibronectin type I repeat homology <1F11>  
F;2174-2209/Domain: fibronectin type I repeat homology <1F12>  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;3/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of fibrin) #status experime  
F;21-47, 45-56, 66-94, 92-104, 110-138, 136-148, 155-184, 182-194, 200-229, 227-239, 277-304, 302-3  
7, 2155-2167, 2174-2200, 2198-2209/Disulfide bonds: #status predicted





J. Biol. Chem. 268, 12812-12817, 1993  
A;Title: Topological analysis of quinoprotein glucose dehydrogenase in Escherichia coli  
A;Reference number: A45997; MUID:93286127; PMID:8509415  
A;Accession: A45997  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-20 <YAM>  
A;Cross-references: UNIPARC:UPI0000171FB2  
R;Fujita, N.  
submitted to the EMBL Data Library, January 1994  
A;Reference number: S45181  
A;Accession: S45201  
A;Molecule type: DNA  
A;Residues: 1-796 <FUJ>  
A;Cross-references: UNIPARC:UPI0000129320; EMBL:D26562; NID:g473770; PIDN:BAA05580.1; PI  
R;Yamada, M.; Asaoka, S.; Saier, M.H.; Yamada, Y.  
J. Bacteriol. 175, 568-571, 1993  
A;Title: Characterization of the gcd gene from Escherichia coli K-12 W3110 and regulatio  
A;Reference number: I41228; MUID:93123180; PMID:8419307  
A;Accession: I41228  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-148, 'H', 150, 'KRRCHT', 157-192, 'K', 194-665, 'H', 667-796 <RES>  
A;Cross-references: UNIPARC:UPI000016F19A; GB:D12651; NID:g216555; PIDN:BAA02174.1; PID:  
C;Genetics:  
A;Gene: gcd  
A;Map position: 3 min  
C;Function:  
A;Description: catalyzes the oxidation of D-glucose to D-gluconic acid by ubiquinone  
A;Pathway: respiratory chain  
C;Superfamily: glucose/alcohol /Shikimate dehydrogenase  
C;Keywords: oxidoreductase; pyrroloquinoline quinone; respiratory chain; transmembrane p  
F;11-37/Domain: transmembrane #status predicted <TM1>  
F;41-59/Domain: transmembrane #status predicted <TM2>  
F;63-81/Domain: transmembrane #status predicted <TM3>  
F;96-110/Domain: transmembrane #status predicted <TM4>  
F;120-140/Domain: transmembrane #status predicted <TM5>  
F;93,95/Binding site: ubiquinone (Arg, Asp) #status predicted  
F;466/Active site: Asp #status predicted

Query Match 5.7%; Score 99; DB 1; Length 796;  
Best Local Similarity 22.3%; Pred. No. 4.8;  
Matches 90; Conservative 44; Mismatches 133; Indels 136; Gaps 24;  
QY 8 LFLIATTRG---WSTD---EANTYFKEWTC-----SSPSLPRSCKEIKDECPS 50  
Db 236 LFALDAASGKEKWHYDPELKTNESFQHVTCRGVSYHEAKAETASP-----EVMADCPR 288  
QY 51 AF-----DG-LYFLRTENGVIYQTFCDMTSGGGGWTLVASVHEND----- 89  
Db 289 RIILPVNDGRLIAINAENGKLCETFANK---GVNLQSNMPDTKPGLYEPTSPPIITDK 344  
QY 90 ---MRGKCTVGDWRWSSQQGSKA----DYPEGDNWANYNTFGSAEAATSDDYK----- 135  
Db 345 TIVMAGSVT--DNFSTRETSGVIRGFDVNTGELLWAFDPGAKDPNAIPSDHFTFNNSPN 402  
QY 136 --NPGYYDIQAKDLGIWHVP-----NKSPMQHWRNSSLLRYRTDTGFL-----QT 178  
Db 403 SWAPAAAYDAK---LDLVLPMGVTTDPDIWGNRTPEQERYASSILALNATGKLAWSYQT 459  
QY 179 LGHNLFGI-----YQKYPVKYGEKGCWTDN-----GPVIPVV 210  
Db 460 VHDLWMDLPAQPTLADITVNGQKVPVIYAPAK--TGNIFVLDNRNGELVVPAPEKPPV 517  
QY 211 YDFGDAQKTASYSPYQOREFTAGF--VQFRVFNNERAANALCAGM-RVTCNTEHHICIG 267  
Db 518 Q--GAAK--GDYVTP-----TQPFSELSFRPTKDLGSGADMWGATMFDQLVCRVMFHQMR 567  
QY 268 GGGYPPEASPOQC-----GDFSFGDWSGYGTHVGYSSSREITEA 306  
Db 568 YEGIFTPPSEQGTLVFPGNLGMFEWGG-----ISVDPNREVAIA 606

RESULT 13  
H90644  
glucose dehydrogenase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509)  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 05-Oct-2004  
C;Accession: H90644  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G  
Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: H90644  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-796 <HAY>  
A;Cross-references: UNIPROT:Q8X946; UNIPARC:UPI00000D0879; GB:BA000007; PIDN:BAB33551.1;  
A;Experimental source: strain O157:H7, substrain RIMD 0509952  
C;Genetics:

RESULT 12  
H85495  
glucose dehydrogenase [imported] - Escherichia coli (strain O157:H7, substrain EDL933)  
C;Species: Escherichia coli  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 05-Oct-2004  
C;Accession: H85495  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodac  
Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: H85495  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-796 <STO>  
A;Cross-references: UNIPROT:Q8X946; UNIPARC:UPI00000D0879; GB:AE005174; NID:g12512839;  
A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: gcd  
C;Superfamily: glucose/alcohol /Shikimate dehydrogenase

Query Match 5.7%; Score 99; DB 2; Length 796;  
Best Local Similarity 22.3%; Pred. No. 4.8;  
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QY 8 LFLIATTRG---WSTD---EANTYFKEWTC-----SSPSLPRSCKEIKDECPS 50  
Db 236 LFALDAASGKEKWHYDPELKTNESFQHVTCRGVSYHEAKAETASP-----EVMADCPR 288  
QY 51 AF-----DG-LYFLRTENGVIYQTFCDMTSGGGGWTLVASVHEND----- 89  
Db 289 RIILPVNDGRLIAINAENGKLCETFANK---GVNLQSNMPDTKPGLYEPTSPPIITDK 344  
QY 90 ---MRGKCTVGDWRWSSQQGSKA----DYPEGDNWANYNTFGSAEAATSDDYK----- 135  
Db 345 TIVMAGSVT--DNFSTRETSGVIRGFDVNTGELLWAFDPGAKDPNAIPSDHFTFNNSPN 402  
QY 136 --NPGYYDIQAKDLGIWHVP-----NKSPMQHWRNSSLLRYRTDTGFL-----QT 178  
Db 403 SWAPAAAYDAK---LDLVLPMGVTTDPDIWGNRTPEQERYASSILALNATGKLAWSYQT 459  
QY 179 LGHNLFGI-----YQKYPVKYGEKGCWTDN-----GPVIPVV 210  
Db 460 VHDLWMDLPAQPTLADITVNGQKVPVIYAPAK--TGNIFVLDNRNGELVVPAPEKPPV 517  
QY 211 YDFGDAQKTASYSPYQOREFTAGF--VQFRVFNNERAANALCAGM-RVTCNTEHHICIG 267  
Db 518 Q--GAAK--GDYVTP-----TQPFSELSFRPTKDLGSGADMWGATMFDQLVCRVMFHQMR 567  
QY 268 GGGYPPEASPOQC-----GDFSFGDWSGYGTHVGYSSSREITEA 306  
Db 568 YEGIFTPPSEQGTLVFPGNLGMFEWGG-----ISVDPNREVAIA 606

RESULT 13  
H90644  
glucose dehydrogenase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509)  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 05-Oct-2004  
C;Accession: H90644  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G  
Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: H90644  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-796 <HAY>  
A;Cross-references: UNIPROT:Q8X946; UNIPARC:UPI00000D0879; GB:BA000007; PIDN:BAB33551.1;  
A;Experimental source: strain O157:H7, substrain RIMD 0509952  
C;Genetics:



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